Prosity: May 19, 1999

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protein search, using sw model OM protein April 28, 2005, 13:57:35 ; Search time 122.5 Seconds (without alignments) 56.830 Million cell updates/sec Run on:

US-10-009-317A-32

116 1 GFCRCICTRGFCRCICTR 18 Title: Perfect score:

Scoring table: Sequence:

2105692 seqs, 386760381 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

A_Geneseq_16Dec04:* Database :

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1980s:* geneseqp1990s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SCHILLES	DB ID Description	4 AAB35046 Aab35046 Theta	5 ABP53295 Anti-vira		8 ADO35240 Ado35240 Rhesus	5 ABP53299 Anti-vira	4 AAB35030 Aab35030 Theta def	5 ABP53297 Anti-vira	6 AAE33866 Macaca	_	ADD35357 Add35357	_	AD035229	AD035238	8 AD035239 Rhesus	8 AD035250 Ado35250 Rhesus	8 AD035263 Ado35263 Monkey	AD035255 Ado35255 1	6 AAE33805 Aae33805 12Y retro	6 AAE33806 Aae33806 IllY retr	8 ADNO8180 Adno8180 Human ret	8 ADN08181 Adn08181 Human ret	4 AAB35037 Aab35037 Rhesus	5 ABP53294 Synthetic	
	Query Match Length D	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	38	18	18	18	18	18	18	18	18
ok	Query Match	100.0	100.0	100.0	95.7	88.8	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	86.2	80.2	80.2	80.2	80.2	78.4	77.6	77.6
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ADN08176 AB035249 AB035249 AA031017 AAE33864 AAN08177 AAB532647 AAB532647 AD035241 AAB33803 AM08179 AM08179 AM08179	AAE33807 ADO35246 ADO35245
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ALIGNMENTS

The present invention provides theta defensin peptides and analogues which have antimicrobial activity. They can be used in the treatment of bacterial, viral, fungal, protozoan and helminthic infections, in dislifectants and as food preservatives Theta defensin; antimicrobial; cyclic; bacterium; fungus; protozoan; virus; helminth; disinfectant; food preservative; analogue. Novel theta defensin peptide with antimicrobial activity against bacteria, yeast, fungi, protozoa and viruses. Ouellette AJ; AAB35046 standard; peptide; 18 AA Claim 15; Fig 16; 110pp; English. Selsted ME, Tang Y, Yuan J, 99US-00309487. rheta defensin SEQ ID NO: 30. 10-MAY-2000; 2000WO-US012842. (REGC) UNIV CALIFORNIA. WPI; 2001-031853/04. WO200068265-A1. 10-MAY-1999; Unidentified. 27-MAR-2001 16-NOV-2000. AAB35046; AAB35046 ID AAB3

Sequence 18 AA;

ö Gaps ö Query Match 100.0%; Score 116; DB 4; Length 18; Best Local Similarity 100.0%; Pred. No. 8.5e-06; Matches 18; Conservative 0; Mismatches 0; Indels

g 8

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GPCRCICTRGFCRCICTR 18
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antimicrobial, antiinflammatory; antibacterial; virucide; fundicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection;

fungal infection; haemolytic activity

Macaca mulatta.

Key Modified-site

Location/Qualifiers

Monkey; Rhesus theta defensin; RTD-2; antimicrobial peptide; cyclic;

Rhesus theta defensin peptide, RTD-2.

15-JUL-2004 (first entry)

AD035230;

ADO35230 standard; peptide; 18 AA

AD035230

Anti-viral, viral infection, theta-defensin, lipid environment, amphipathic alpha-helical structure, virucide, anti-HIV, immunisation, viral growth inhibitor, viral proliferation inhibitor. New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus. 'n Maury W, Stapleton J, Stinski M, Roller R, Mccray PB, Tack Anti-viral theta defensin peptide RTD-2 SEQ ID NO:28. Disclosure; Page 10; 65pp; English. ABP53295 standard; peptide; 18 AA 29-JAN-2002; 2002WO-US002435. 30-JAN-2001; 2001US-0265270P. 01-AUG-2001; 2001US-0309368P. (IOWA) UNIV IOWA RES FOUND (first entry) WPI; 2002-674815/72. Macaca mulatta. WO200260468-A2. 13-NOV-2002 amphipathic viral growth 08-AUG-2002 Synthetic ABP53295; RESULT 2 ABP53295

The present invention describes a method (MI) of using a first anti-viral peptide (I) comprising a theta-defensin peptide in an amphipathic alphahelical structure in a lipid environment for reducing the infectivity of a virus. (I) can have viruled and anti-HIV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of anti-viral tesistance. (I) can be used for inhibiting the growth and proliferation of a virus and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent viral proliferation in a subject harbouring a latent virus, controlling virus is spread within a virally-infected subject (VS), reducing virus latent virus, controlling virus spread within a virally-infected subject (VS), reducing virus badd from a VS, reducing percentage of VS in a vis, (b) reducing the infectivity of a virus; and (c) rendering virus of virus and (c) rendering virus of infectious virus particles in a population of viruses. (MI) is useful for reducing the infectivity of a virus in sheep, cattle, horses, whine, cats, fowl and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is administered prior to or subject to the virus contacting the subject.

The anti-viral peptide is most preferably administered to a subject who is for the virus of is chronically, latently or acutely infected with the virus. The present sequence represents a rhesus monkey theta defensin anti-viral peptide, which is given in the exemplification of the present invention

The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as AD035239-AD035257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., context lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The poptices are also useful for decreasing inflammatory response and for microbicidal inhibition of growth. Thus the peptides are useful as the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensing have ö bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents the rhesus monkey wild-type theta defensin RTD-2. Novel theta defensin analog useful for reducing or inhibiting growth survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate 18 //note= "The peptide is cyclised by a covalent link between these two residues" Example 1; SEQ ID NO 2; 46pp; English. 30-APR-2003; 2003US-00427715. 30-APR-2002; 2002US-0377071P. (REGC) UNIV CALIFORNIA. 3. .16 5. .14 7. .12 Selsted ME, Tran DQ WPI; 2004-167945/16. Disulfide-bond Disulfide-bond JS2004014669-A1 Disulfide-bond 22-JAN-2004. object.

Sequence 18 AA;

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Gaps

Length 18; 100.0%; Score 116; DB 8; 100.0%; Pred. No. 8.5e-06; Query Match Best Local Similarity

Matches

Sequence 18 AA;

1 GFCRCICTRGFCRCICTR 18

18; Conservative

; 0 100.0%; Score 116; DB 5; Length 18; 100.0%; Pred. No. 8.5e-06; Indels ; 0; Mismatches Query Match Best Local Similarity

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                                                                                                                                                                       Monkey, Rhesus theta defensin, RTD; antimicrobial peptide, antimicrobial, antinflammatory; antibacterial; virucide, fungicide, food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant;
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 Gaps
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 0; Indels
                                                                                                                                                                                                                food preservative, bacterial infection, viral infection, fungal infection, haemolytic activity.
                                                                                                                                                     Rhesus theta defensin analogue peptide aRTD-2-OH.
Mismatches
                                                                                                                                                                                                                                                                                                                                  /note= "Hydroxylated"
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0;
                                                                                         ADO35240 standard; peptide; 18
                                GFCRCICTRGFCRCICTR 18
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                    GFCRCICTRGFCRCICTR
                                                                                                                                 (first entry)
18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tran DQ;
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Disulfide-bond
Disulfide-bond
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                                                                                                                                                                                                                                                 Macaca mulatta
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                                                                                                            AD035240;
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Matches
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The present invention describes a merical variable and properties of the present invention describes a merical service and problems and peptide in an amphipathic alphabalical structure in a lipid environment for reducing the infectivity of a virus. (I) can have virucide and anti-HIV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of anti-HIV activity burden, shed, and development of anti-Viral resistance. (I) can be used for inhibiting the growth and control problems and a virus and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent virus for infection in a subject harbouring a latent virus, controlling virus shed from a Viral infection gratus, or inducing virus status or virus shed from a Viral infection status, or inducing virus contaminated tissue or fluid sample safe for use, or reducing the number of virus particles in a population of viruses. (MI) is useful of infectious virus particles in a population of viruses, whine, cot infectious virus particles in a population of viruses, where the first anti-viral peptide is contaministered to a patient who is immunosuppressed or to a subject who is administered prior to or subsequent to the virus on the virus of a subject. The anti-viral peptide is administered prior to or subsequent to the virus of a subject who is contaminated virus. The present contamination represents a chimeric human/rhesus monkey theta defensin anti-viral peptide is sequence represents a chimeric human/rhesus monkey theta defensin anti-
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                                                                                                                                                                                                                                                                                                                                                                                              Anti-viral; viral infection; theta-defensin; lipid environment; amphipathic alpha-helical structure; virucide; anti-HIV; immunisation; viral growth inhibitor; viral proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus.
                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                           Anti-viral chimeric theta defensin peptide H/RTD-2 SEQ ID NO:32
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  Score 111; DB 8; Length 18
Pred. No. 2.8e-05;
; Mismatches 1; Indels
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01-AUG-2001; 2001US-0309368P.
Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                  1 GFCRCICTRGFCRCICTR
                                                                                                                           1 GPCRCTCTRGFCRCICTR
                                                                                                                                                                                                                                                                                                                    13-NOV-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO35257. The theta defensin analogue is useful for reducing or inhibiting growth or survival

of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of growth. Thus the peptides are useful as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present

sequence represents a Rhesus theta defensin analogue peptide

Sequence 18 AA

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Anti-viral; viral infection; theta-defensin; lipid environment; amphipathic alpha-helical structure; virucide; anti-HIV; immunisation; viral growth inhibitor; viral proliferation inhibitor.
                                                   Anti-viral theta defensin peptide RTD-1 SEQ ID NO:30.
ABP53297 standard; peptide; 18 AA.
                                   13-NOV-2002 (first entry)
                                                                                                        Macaca mulatta.
                                                                                                                                                   08-AUG-2002
                                                                                                                Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides theta defensin peptides and analogues which have antimicrobial activity. They can be used in the treatment of bacterial, viral, fungal, protozoan and helminthic infections, in
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                                                             Gaps
                                                                                                                                                                                                                 fungus; protozoan; analogue.
viral peptide, which is given in the exemplification of the present
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bacteria, yeast, fungi, protozoa and viruses.
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3..16
5..14
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                                            Length 18;
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                                                            2; Indels
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Pred. No. 0.00032;
1; Mismatches 2;
                                          Score 103; DB 5;
Pred. No. 0.0002;
); Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                 Ouellette AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bacterial, viral, fungal, protozoan and
disinfectants and as food preservatives
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                                                                                                                                           AAB35030 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.1%;
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                                           88.8%;
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                                                                                               GICRCICTRGFCRCICGR
                                                                                                                                                                                               Theta defensin SEQ ID NO: 1.
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Best Local Similarity 83...
Best Local 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-031853/04.
                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                            Unidentified
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                                                                                                                                                                                                                                                                                                                                           16-NOV-2000.
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         invention
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                                                             Matches
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The present invention describes a method (M1) of using a first anti-viral peptide (I) comprising a theta-defensin peptide in an amphipathic alphabelia beliaci structure in a lipid emvironment for reducing the infectivity of a virus. (I) can have virucide and anti-HIV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of anti-viral tresistance. (I) can be used for inhibiting the growth and proliferation of a virus and so can be used for; (a) proceeding or treating subject from a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling virus spread within a virally-infected subject (VS), reducing virus budget harbouring a latent virus, controlling virus shed from a VS, reducing percentage of VS in a contaminated tissue or fluid sample safe for use, or inducing latency in a VS, in educing virus particles in a population of viruses. (M1) is useful for infectious virus particles in a population of viruses (M1) is useful for infectious virus particles in a population of viruses. (M1) is useful for reducing the infectivity of a virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is a dainistered prior to or subsequent to the virus contacting the subject. Who is containistered to a patient who is immunosuppressed or to a subject who is containistered to a patient who is immunosuppressed to a subject who is containistered to a patient who is immunosuppressed or case subject who is containistered to a patient who is immunosuppressed to a subject who is containistered to a patient who is immunosuppressed or case subject who is containistered to a patient who is immunosuppressed or case subject who is containistered to a patient who is immunosuppressed or case subject who is containistered prior to or subsequent to the virus contacting the subject. Who is chronically, latently or acutely infected with the virus present sequence represents a rhesus monkey thete defensin anti-viral pep
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Pred. No. 0.00032;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mccray PB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maury W, Stapleton J, Stinski M, Roller R,
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01-AUG-2001; 2001US-0309368P,
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Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              (IOWA ) UNIV IOWA RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-674815/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18 AA;
WO200260468-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
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RESULT 7 ABP53297

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Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
ADD35357
The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is rhesus monkey theta defensin, RTDI peptide. This sequence is used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bacterial infection; human pathogen; holin; defensin;
peptide nucleic acid; PNA; penicillin; tetracycline; ampicillin;
kanamycin; antibiotic; antibacterial; antibiotic-resistance gene; cyclic.
                                                                                                 Retrocyclin, infection, sexually transmitted disease, gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; rhesus monkey; theta defensin 1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                      New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 101; DB 6; Lengtu L. Pred. No. 0.00032;
                                                                                                                                                                                                                                                                              Hong TB;
                  AAE33866 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                              Lehrer RI, Waring AJ, Cole AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ź
                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 3C; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADD95202 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.1%;
                                                                                                                                                                                                                 18-APR-2002; 2002WO-US012353.
                                                                                                                                                                                                                                      18-APR-2001; 2001US-0284855P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GFCRCICTRGFCRCICTR
                                                                               Macaca mulatta RTD1 peptide
                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyclic defensin fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                  WPI; 2003-103387/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18 AA;
                                                                                                                                                     Macaca mulatta
                                                                                                                                                                       WO200285401-A1
                                                           16-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2004
                                                                                                                                                                                             31-0CT-2002
                                      AAE33866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADD95202;
                                                                                                                                  RIDI.
        AAE33866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
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This invention describes a novel conjugate for treating prokaryotic infections which comprises a transport mediator for passage through the prokaryotic cell membrane and a compound, directed against a prokaryote and intended for introduction into it. The prokaryote is a bacterium, especially one pathogenic in humans. The transport mediator is preferably of human peptide or protein, especially a phage-holin protein, its active fragment or variant or a defensin. The introduced compound is a peptide nucleic acid (PNA) that inhibits a gene, especially one implicated in cenistance to penicillin, tetracycline, ampicillin or knammycin. The conjugate has the structure transport mediator-spacer-PNA where the spacer is poly(glycine and/or lysine), preferably containing 2-6 amino cidas and the spacer is linked to the transport mediator through a cleavable disulfide bridge. The conjugates are administered together with an antibiotic, by parenteral, transdermal or subcutaneous routes. The conjugates are administered together with especially in combination with antibiotics, for treating prokaryotic, specifically bacterial, infections, especially where the pathogen is cresistant to at least one antibiotics and then the PNA is directed against the antibiotic-resistance gene. Where the PNA is directed against containing the condaministered antibiotics in antibiotics can be enabled the invention and enthe pna is contained to a condaministered antibiotics i.e. 'Old' antibiotics can be enabled the invention when antibiotics and be instituted to co-administered antibiotics i.e. 'Old' antibiotics and personal in the condamination where the prace is an interest of the antibiotics and becreain when antibiotics and pare man antibiotics and the institute the parenter when antibiotics and the place whe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New conjugate of transport mediator and active agent, useful for treating prokaryotic infections, especially by neutralizing antibiotic resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used successfully in cases where normally they would be ineffective. This sequence represents a cyclic defensin fragment described in the

    .18
/note= "Residue 1 and residue 18 bond to form a cyclic

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waldeck W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 0.00
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Braun K, Braun I, Debus J, Pipkorn R,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADD35357 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 10; 34pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GFCRCICTRGFCRCICTR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JAN-2003; 2003WO-DE000124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JAN-2002; 2002DE-01001862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPCRCLCRRGVCRCICTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                       moiety"
                                                                                                                                                                                        3. .16
5. .14
7. .12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-689464/65.
    Key
Misc-difference
                                                                                                                                                                                   Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                           WO2003059392-A2
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Gerdes

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for preparing a composition for treatment and/or prevention of bacteraemia for binding bacterial products such as lipopolysaccharide (LPS) and/or lipteichonic acid (LTA), or for treatment and/or prevention of septic shock. RTD-1, isolated from immune cells of rhesus monkeys, has antibacterial, fungicide, virucide, immunomodulator and anticoagulant activity. RTD-1 inhibits microbial cell-all biosynthesis and also binds to LPS and LTA. RTD-1 is useful for treatment and prevention of severe infections caused by Gram-positive or -negative bacteria and yeasts, or antimicrobial action, neutralisation of bacterial products (by binding), immunomodulation (reducing release of proinflammatory cytokines but increasing release of regulatory factors) and anticoagulant action, so
                                                                                                                                                                                                                                                            Use of rhesus theta defensin-1 for treating or preventing bacteremia and septic shock, also for binding bacterial products and as immunomodulator and anticoagulant.
                                                                                                                                                                                                                                                                                                                                                                                             This invention describes the novel use of rhesus theta defensin-1 (RTD-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monkey, Rhesus theta defensin, RTD-1; antimicrobial peptide; cyclic; antimicrobial; antiinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection; haemolytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .18 /note= "The peptide is cyclised by a covalent link between these two residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.1%; Score 101; DB 8; Length 18;
83.3%; Pred. No. 0.00032;
cive 1; Mismatches 2; Indels
                                                                                                                                                                          Newton B, Labischinski H, Brunner N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                provides a better and simpler treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhesus theta defensin peptide, RTD-1.
                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID NO 1; 28pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADO35229 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
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                                           30-MAY-2003; 2003WO-EP005694.
                                                                                    13-JUN-2002; 2002DE-01026216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GFCRCLCRRGVCRCICTR
                                                                                                                               (FARB ) BAYER HEALTHCARE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3. .16
5. .14
7. .12
                                                                                                                                                                                                                 WPI; 2004-071500/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Macaca mulatta.
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Modified-site
24-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AD035229;
                                                                                                                                                                          Ladel C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel ophthalmic solution comprising a prostaglandin of the F-series and an antimicrobial peptide. A solution of the invention has hypotensive and ophthalmological activity. The solution is useful for the treatment of increased intracular pressure, such as caused by glaucoma and for the reduction of coular hypertension. The prostaglandin and the antimicrobial peptide work synergistically, to provide beneficial reduction in the incidence of irritant and toxic side effects such as hyperaemia, irritation and inflammation of conjunctiva, evelar cell dysplasia, iridial melanocyte hyperplasia, and hyperplamentation, associated with the prior art prostaglandin compositions. The present sequence represents an antimicrobial peptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rhesus theta defensin-1; RTD-1; bacteraemia; lipopolysaccharide; LPS; lipiteichonic acid; LTM; septic shock; antibacterial; fungicide; virucide; immunomodulator; anticoagulant activity; microbial cell-wall biosynthesis; immunomodulation; anticoagulant.
                                                             antimicrobial; ophthalmic; prostaglandin; hypotensive; ophthalmological; intraocular pressure; glaucoma; ocular hypertension; hyperaemia; irritation; inflammation; conjunctiva; ocular cell dysplasia; iridial melanocyte hyperplasia; hyperpigmentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treatment of increased intraocular of the F-series and an antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 101; DB 8; Length 10
Pred. No. 0.00032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhesus theta-defensin-1 (RTD-1) peptide.
                    Antimicrobial peptide theta-defensin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ophthalmic solution useful for the pressure comprises a prostaglandin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 11, 11pp, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ¥.
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                                                                                                                                                                                                                                                                                                                                                    21-MAR-2002; 2002US-0367071P.
                                                                                                                                                                                                                                                                                                         21-MAR-2003; 2003WO-US008935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GFCRCLCRRGVCRCICTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GFCRCICTRGFCRCICTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                (CAYM-) CAYMAN CHEM CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Johnson J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-011506/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
es 15; Conserv
                                                                                                                                                                                                                     WO2003079997-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003105883-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca mulatta
                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAR-2004
                                                                                                                                                                                                                                                                02-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                         Maxey KM,
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Matches

RESULT 11

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Monkey, Rhesus theta defensin, RTD; antimicrobial peptide, antimicrobial, antinflammatory, antibacterial, virucide, fungicide, food, contact lens solution, eye wash solution, inflammatory response, microbicidal inhibition, microbistatic growth inhibition; disinfectant, food preservative, bacterial infection, viral infection, thempal infection, haemolytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhesus theta defensin analogue peptide aRTD-1-NH.
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Matches 15; Conservative
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Disulfide-bond
Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO35257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents the rhesus monkey wild-type theta defensin RTD-1.
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                                                                                                                                                                                                                                                                                      Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
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Pred. No. 0.00032;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhesus theta defensin analogue peptide aRTD-1-OH.
                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; SEQ ID NO 1; 46pp; English.
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                                                  30-APR-2003; 2003US-00427715.
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83.3%;
                                                                                            30-APR-2002; 2002US-0377071P
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                                                                                                                                         (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                           WPI; 2004-167945/16.
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Disulfide-bond
Disulfide-bond
Modified-site
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  22-JAN-2004.
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                                                                                                                                                                                            Selsted ME,
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18 18

1 GPCRCICTRGFCRCICTR 1 GFCRCLCRRGVCRCICTR

15-JUL-2004 (first entry)

Location/Qualifiers

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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as AD03529-AD035257. The theta defailed in the claims or appearing as AD03529-AD035257. The theta defailed in the claims or appearing as AD03529-AD035257. The theta is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or cod product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
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83.3%; Pred. No. 0.00032;
ive 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                   30-APR-2002; 2002US-0377071P.
                                                                                                                                                                                                                                                                                                                                                                                  (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Selsted ME, Tran DQ;
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US2004014669-A1.
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                                                                                               22-JAN-2004
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Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO3527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have sign antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.
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                                                                                                                                                                                                                                                                                                                            Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
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                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 13; 46pp; English
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                                       /note= "Amidated"
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                                                                                                                                                                                  30-APR-2002; 2002US-0377071P.
                                                                                                                                              30-APR-2003; 2003US-00427715
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                                                                                                                                                                                                                                                         Tran DQ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 AA;
Disulfide-bond
Modified-site
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                                                                                                            22-JAN-2004.
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Matches
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Macaca mulatta Synthetic.

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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO3527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., context lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbistatic inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for the action. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.
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    18
/note= "The peptide is cyclised by a covalent link
between these two residues"

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Pred. No. 0.00032;
); Mismatches 2; Indels
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Matches 16; Conservative
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                                                                                                                              3. .16
5. .14
7. .12
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                                                                                                                      Disulfide-bond
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Disulfide-bond
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US-09-309-487-1
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                                                                                                                                                     April 28, 2005, 14:12:37 ; Search time 30 Seconds (without alignments) 44.789 Million cell updates/sec
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Sequence 8
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(c) 1993 - 2005 Compugen Ltd
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ALIGNMENTS

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APPLICANT: Selsted, Michael E.
APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Tang, Yi-Quan
APPLICANT: Tang, Yi-Quan
APPLICANT: Tang, Man, Jun
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REPERENCE: P-UC 3095
CURRENT APPLICANT: NUMBER: US/09/309,487
CURRENT FILING DAITE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO I
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Sequence 1, Application US/09967808

Patent No. 6514727

GENERAL INFORMATION:

APPLICANT: Seleced, Michael E.

APPLICANT: Tang, Yi-Quan

APPLICANT: Tang, Yi-Quan

APPLICANT: Tang, Yi-Quan

TITLE OF INVENTION: Same

TITLE OF INVENTION: Same

TITLE OF INVENTION: Same

CURRENT PILING DATE: 2001-09-26

FILE REPERBENCE: P-UC 3095

CURRENT PILING DATE: 1999-05-10

PRIOR APPLICATION NUMBER: US/09/309,487

PRIOR FILING DATE: 1999-05-10

NUMBER OF SEQ ID NOS: 31

SOFTHARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 18
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Sequence 1, Application US/09309487
Patent No. 6335318
GENERAL INFORMATION:
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, ORGANISM: Macaca mulatta
US-09-309-487-1
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Best Local Similarity
Matches 15; Conserv
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Sequence 9, Application US/09309487
Patent No. 6335318
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Tang, Yi-Quan
APPLICANT: Tang, Andre J.
TITLE DF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REFERENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 9
SEQ ID NO 9
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Sequence 9, Application US/09967808

Patent No. 6514727

GENERAL INFORMATION:

APPLICANT: Selsted, Michael E.

APPLICANT: Tang, Yi-Quan

APPLICANT: Vuan, Jun

APPLICANT: Vuan

APPLICANT: Vuan

APPLICANT: Vuan

APPLICANT: Vuan

APPLICANT: Vuan

FILE REFERENCE: P-UC 3095

CURRENT APPLICATION NUMBER: US/09/309,487

PRIOR FILING DATE: 1999-05-10

NUMBER OF SEQ ID NOS: 31

SEQ ID NO 9

SEQ ID NO 9
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80.2%; Score 93; DB 4; I
Best Local Similarity 77.8%; Pred. No. 0.00011;
Matches 14; Conservative 1; Mismatches 3;
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Best Local Similarity 81.2%; Pred. No. 0.00018;
Matches 13; Conservative 1; Mismatches 2;
                                                      ; OTHER INFORMATION: synthetic variant US-10-141-645-6
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ORGANISM: Artificial Sequence
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US-09-967-808-9
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US-09-309-487-9
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                                                                                                                                     Query Match 87.1%; Score 101; DB 4; Length 18; Best Local Similarity 83.3%; Pred. No. 1.4e-05; Matches 15; Conservative 1; Mismatches 2; Indels
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GENERAL INCOMMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan waring
APPLICANT: Alexander Cole
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
ITILE OF INVENTION: Retrocyclins - Antiviral and
ITILE OF INVENTION: Retrocyclins - Antiviral
ITILE OF INVENTION: Retrocyclins - Antiviral and
ITILE OF INVE
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APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FIRE REPERENCE: UCLA-001CIP
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CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR PLILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 18
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US-10-141-645-5
'Sequence 5, Application US/10141645
'Patent No. 6713078
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ORGANISM: Artificial Sequence
                                ; ORGANISM: Macaca mulatta
US-09-967-808-1
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Length 18;
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Patent No. 6713078

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001C1P
FILE REPERENCE: UCLA-001C1P
CURRENT PILING DATE: 2002-05-06
PRIOR PRILING DATE: 2001-04-18
FRIOR APPLICATION NUMBER: Unassigned
PRIOR FILING DATE: 2001-04-18
FRIOR APPLICATION NUMBER: Unassigned
FRIOR PRILING DATE: 2001-04-18
FRIOR SEQ ID NOS: 125
SOFTWARE: PastSEQ for Windows Version 4.0
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APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: 2002-05-06
FILE REFERENCE: 2002-05-06
PRIOR APPLICATION NUMBER: 00/284,855
PRIOR APPLICATION NUMBER: 00/284,855
PRIOR APPLICATION NUMBER: 00/284,855
PRIOR APPLICATION NUMBER: Uses 00/284,855
NUMBER OF SEQ 1D NOS: 125
SOFTWARE: PRECED 10 NOS: 125
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Pred. No. 0.00085;
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; OTHER INFORMATION: synthetic variant
US-10-141-645-2
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CTHER INFORMATION: synthetic variant
US-10-141-645-3
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ORGANISM: Artificial Sequence
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Best Local Similarity 72.4.
Best Local 3; Conservative
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Best Local Similarity 72.2
Matches 13; Conservative
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                                    RESULT 9
US-10-141-645-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan Waring
TITLE OF INVENTION: Retrocyclins - Antiviral
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT APPLICATION NUMBER: 60/284,855
PRIOR APPLICATION NUMBER: 60/284,855
PRIOR APPLICATION NUMBER: Unassigned
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 125
SEQ TONO:
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SEQ TONO:
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Pred. No. 0.00023;
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CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2001-05-15
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; Sequence 53, Application US/09917340
; Patent No. 6696238
                                                                                                                                                                                          Sequence 1, Application US/10141645
Patent No. 6713078
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77.8%;
3 GFCRCLCRRGVCRCIC 18
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 53
LENGTH: 18
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Best Local Similarity 77.8
Matches 14; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
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ORGANISM: Homo sapiens
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OTHER INFORMATION: synthetic variant US-10-141-645-9
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; OTHER INFORMATION: synthetic variant
US-10-141-645-8
                                                                                   US-10-141-645-8; Sequence 8, Application US/10141645; Patent No. 6713078
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1 GICYCICGRGICRCICGR 18
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ORGANISM: Artificial Sequence
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Best Local Similarity 66.7%;
Matches 12; Conservative
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US-10-141-645-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/10141645;
Patent No. 6713078;
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan Waring
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT PILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/284,855
PRIOR APPLICATION NUMBER: Unassigned
PRIOR APPLICATION NUMBER: Unassigned
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SEQTHARE: FastSEQ for Windows Version 4.0
ILENGTH: 18
                                                                                                                               APPLICANT: Robert Lehrer
APPLICANT: Robert Lehrer
APPLICANT: Alexander Cole
APPLICANT: Alexander Cole
APPLICANT: Alexander Cole
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT APPLICATION NUMBER: 60/284,855
PRIOR APPLICATION NUMBER: 1002-05-06
PRIOR PILING DATE: 2001-04-18
FRIOR PILING DATE: 2001-04-18
FRIOR PILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SEQ ID NO 4
LEMEGTH: 18
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                                                                                      Sequence 4, Application US/10141645 Patent No. 6713078
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Matches 13; Conservative
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US-10-141-645-7
                                             RESULT 11
US-10-141-645-4
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APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Tacsaa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
TILLE OF PREBRICE: 2002-05-06
PRIDE REPREBRICE: 2002-06-06
PRIOR PRILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: Unassigned
PRIOR PILING DATE: 2002-04-18
PRIOR PILING DATE: 2002-04-18
SEQ ID NOS: 125
SOFTWARE: FRAEEQ for Windows Version 4.0
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APPLICANT: Alan Waring
APPLICANT: Alaxander Cole
APPLICANT: Alexander Cole
APPLICANT: Alexander Cole
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: US/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2002-04-18
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Pred. No. 0.011;
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SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 18
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2: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{pubpaa} \( 1
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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					SUMMARIES	
Result		*				
No.	Score	Match	Match Length DB	DB	OI	Description
	116	100.0	18	14	US-10-060-102-28	Sequence 28, Appl
7	116	100.0	18	15	US-10-427-715-2	Sequence 2, Appli
٣	116	100.0	18	15	US-10-427-715-14	
4	116	100.0	18	15	US-10-721-839-28	Sequence 28, Appl
2	103	88.8	18	14	US-10-060-102-32	
9	103	88.8	18	15	US-10-721-839-32	Sequence 32, Appl
7	101	87.1	18	14	US-10-060-102-30	
œ	101	87.1	18	14	US-10-313-994-1	1
6	101	87.1	18	15	US-10-427-715-1	٦,
10	101	87.1	18	15	US-10-427-715-12	٠.
11	101	87.1	18	15	US-10-427-715-13	-
12	101	87.1	18	15	US-10-427-715-24	Sequence 24, Appl
13	101	87.1	18	15	US-10-721-839-30	

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Sequence 29, Appli Sequence 5, Appli Sequence 6, Appli Sequence 17, Appli Sequence 27, Appli Sequence 23, Appli Sequence 23, Appli Sequence 31, Appli Sequence 31, Appli Sequence 29, Appli Sequence 15, Appli Sequence 16, Appli Sequence 17, Appli Sequence 29, Appli	38,
5 US-10-427-715-29 4 US-10-141-645-6 4 US-10-141-645-6 4 US-10-313-994-9 4 US-10-313-994-9 4 US-10-141-645-1 5 US-10-427-715-23 6 US-10-427-715-23 7 US-10-909-13-34 10S-09-917-340-53 10S-09-917-340-53 10S-09-917-340-53 10S-09-917-340-53 10S-09-917-340-53 10S-09-917-967 10S-09-918-67 10S-09-918-67 10S-09-918-67 10S-09-918-67 10S-09-918-67 10S-09-918-67 10S-09-918-67 10S-09-918-67 10S-09-918-67 10S-09-918-67 10S-09-918-715-19 10S-09-918-715-19 10S-09-918-715-19 10S-09-918-715-19 10S-09-918-715-19 10S-09-918-715-19 10S-09-918-715-19 10S-09-918-715-19 10S-09-918-715-19 10S-09-918-715-19 10S-09-918-715-28 10S-10-141-645-9 10S-10-141-645-9 10S-10-141-645-9 10S-10-141-645-9 10S-10-141-645-9 10S-10-141-645-9 10S-10-141-645-9 10S-10-141-645-9	US-10-427-71
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ALIGNMENTS

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US-10-060-102-28

Sequence 28, Application US/10060102

APPLICANT: STALEACON.

APPLICANT: STAINSKY, WARK

APPLICANT: STINSKY, WARK

APPLICANT: TRINSKY, WARK

APPLICANT: TRINSKY, WARK

APPLICANT: TRINSKY, WARK

APPLICANT: TACK, BRIAN

TITLE OF INVENTION: OATHELICIDINS

TITLE OF INVENTION: OATHELICIDINS

CURRENT APPLICATION UNMER: 60/309,368

CURRENT APPLICATION NUMBER: 60/309,368

PRIOR FILING DATE: 2001-09-01

PRIOR PILING DATE: 2001-01-30

NUMBER OF SEQ ID NOS: 32

SOUTHWARE: Attificial Sequence

FRATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Peptide

US-10-660-102-28

OWENT MARCH

BEST LOCAL 18; Pred No: 1800 189; Pred No: 18-06; Indels 0; Indels 0; Gaps 0;
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TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALITITLE OF INVENTION: CATHELICIDINS
TITLE OF INVENTION: CATHELICIDINS
FILE OF INVENTION: CATHELICIDINS
FILE OF INVENTION: CATHELICIDINS
FILE OF INVENTION: CATHELICIDINS
FILE OF INVENTION UNMBER: US/10/721,839
CURRENT APPLICATION NUMBER: US/10/660,102
PRIOR APPLICATION NUMBER: US/10/660,102
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-01-30
NUMBER: OF SEQ ID NOS: 32
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Description of Artificial Sequence: Synthetic CTHER INFORMATION: Peptide US-10-721-839-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 116; DB 15; Length 18; 100.0%; Pred. No. 1e-06; Live 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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                        STAPLETON, JACK
ROLLER, RICHARD
STINSKI, MARK
MCCRAY, PAUL B.
TACK, BRIAN
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Best Local Similarity 100.
Matches 18, Conservative
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                                                                                                                                 Sequence 2, Application US/10427715

Publication No. US20040014669A1

GENERAL INFORMATION:

APPLICANT: Selsted, Michael E.

APPLICANT: Tran, Dat Q.

TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs

TITLE OF INVENTION: Thereof, and Methods of Use

FILE REFERENCE: 66778-302 (US5754)

CURRENT APPLICATION NUMBER: US/10/427,715

CURRENT FILING DATE: 2003-04-30

PRIOR FILING DATE: 2002-04-30

NUMBER OF SEQ ID NOS: 41

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 18
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APPLICANT: Selected, Michael E.
APPLICANT: Tran, Dat Q.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analoge
TITLE OF INVENTION: Thereof, and Methods of Use
FILE REFERENCE: 66778-302(UC5754)
CURRENT APPLICATION NUMBER: US/10/427,715
CURRENT FILING DATE: 2003-04-30
PRIOR PLICALION NUMBER: US 60/377,071
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100.0%; Pred. No. 1e-06;
tive 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 18
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1 GFCRCICTRGFCRCICTR 18
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Best Local Similarity 100.0
Matches 18, Conservative
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Matches 18; Conservative
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US-10-427-715-14
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Gaps

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Sequence 32, Application US/10060102

Sequence 32, Application US/10060102

Publication No. US20030022829A1

GENERAL INFORMATION:

APPLICANT: STAPLETON, JACK

APPLICANT: STAPLETON, JACK

APPLICANT: STAPLETON, JACK

APPLICANT: STOLER, RICHARD

APPLICANT: TINSKI, MARK

APPLICANT: TACK, BRIAN

TITLE OF INVENTION: CATHELICIDINS

TITLE REPRENCE: 10WA:035US

FRIOR FILING DATE: 2001-09-01

FRIOR FILING DATE: 2001-01-30

FRIOR FILING DATE: 2001-08-01

FRIOR FILING DATE: 2001-08-01

FRIOR FILING DATE: 2001-08-01

SEQ ID NO 32

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CHER INFORMATION: Description of Artificial Sequence: Synthetic
CHER INFORMATION: Peptide
CS-10-060-102-32
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88.9%; Pred. No. 2.9e-05;
tive 0; Mismatches 2;
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Best Local Similarity 88.9°
Matches 16; Conservative
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SQUENCE 1. Application US/10313994

| SEQUENCE 1. Application VS/10313994
| Publication No. US20030162718A1
| GENERAL INFORMATION:
| APPLICANT: Selected, Michael E.
| APPLICANT: Tang, Yi-Quan
| APPLICANT: Tang, Yi-Quan
| APPLICANT: Tang, Yi-Quan
| APPLICANT: Tang, Yi-Quan
| APPLICANT: Or INVERTION: Andrew J.
| TITLE OF INVERTION: Antimicrobial Theta Defensins and Methods of Using Same
| TITLE OF INVERTION: 2002-12-05
| CURRENT FILING DATE: 1999-05-10
| PRIOR APPLICATION NUMBER: US/09/309,487
| PRIOR FILING DATE: 1999-05-10
| NUMBER OF SEQ ID NOS: 31
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO.
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; ; OTHER INFORMATION: Peptide US-10-060-102-30
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                                                                                                      Length 18
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APPLICANT: Seleced, Michael B.
APPLICANT: Tran, Dat Q.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
FILE REFERENCE: 66778-302(UC5754)
CURRENT APPLICATION UNDRER: US/10/427,715
CURRENT FILING DATE: 2003-04-30
PRIOR FILING DATE: 2002-04-30
                                                                                                                                                    2; Indels
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                                                                                                   Score 101; DB 14;
Pred. No. 4.9e-05;
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Pred. No. 4.9e-05;
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                                                                                                                                                    1; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 1, Application US/10427715
Publication No. US20040014669A1
GENERAL INFORMATION:
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83.38;
                                                                                                   Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
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Best Local Similarity 83.3.
Best Local 15; Conservative
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ORGANISM: Macaca mulatta
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ORGANISM: Macaca mulatta
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                                                                                                                             Sequence 32. Application US/10721839

Sequence 32. Application No. US20040086335A1

GENERAL INFORMATION:

APPLICANT: MAURY, WENDY

APPLICANT: STIRKI, MARK

APPLICANT: STIRKI, MARK

APPLICANT: APPLICANT: ALICHARD

APPLICANT: APPLICANT: ALICHARD

APPLICANT: APPLICANT: ALICHARD

APPLICANT: TACK, BRIAN

TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI

TITLE OF INVENTION: CATHELICIDINS

FILE REFERENCE: 100Ma.035US

CURRENT APPLICATION NUMBER: US/10/721,839

CURRENT PILING DATE: 2003-11-25

PRIOR FILING DATE: 2001-08-01

PRIOR FILING DATE: 2001-08-01

PRIOR FILING DATE: 2001-08-01

PRIOR PILING DATE: 2001-08-01
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APPLICANT: MAURY, WENDY
APPLICANT: STAPLETON, JACK
APPLICANT: STAPLETON, JACK
APPLICANT: STAPLETON, JACK
APPLICANT: STAPLETON, JACK
APPLICANT: STINSKI, MARK
APPLICANT: APPLICANT: APPLICANT: MCRAY, PAUL B.
APPLICANT: APPLICANT: ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALITILE OF INVENTION: CATHELICIDINS
FILE REFERENCE: 100A:035US
CURRENT APPLICATION NUMBER: US/10/060,102
CURRENT APPLICATION NUMBER: 60/309,368
PRIOR FILING DATE: 2001-08-01
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
CTHER INFORMATION: Peptide
US-10-721-839-32
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88.8%; Score 103; DB 15;
Best Local Similarity 88.9%; Pred. No. 2.9e-05;
Matches 16; Conservative 0; Mismatches 2;
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Publication No. US20030022829A1
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
                                                                                                                     -10-721-839-32
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LENGTH: 18
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LENGTH: 18
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US-10-721-839-30

Sequence 30, Application US/10721839

Publication No. US20040086535A1

GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
APPLICANT: STAPLETON, JACK
APPLICANT: STAPLETON, JACK
APPLICANT: STINSKI, MARK
APPLICANT: TACK, BRIAN
ITILE OF INVENTION: CATHELICIDINS
ITILE OF INVENTION: CATHELICIDINS
ITILE OF INVENTION: CATHELICIDINS
ITILE OF INVENTION: UNMBER: US/10/721,839
CURRENT APPLICATION NUMBER: US/10/060,102
FRIOR APPLICATION NUMBER: 60/309,368
FRIOR APPLICATION NUMBER: 60/309,368
FRIOR PILING DATE: 2001-08-01
FRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE PATENTIN VET: 2.1
SEQ ID NO 30
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US-10-721-839-30
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                       Sequence 24, Application US/10427715

Publication No. US20040014669A1

GENERAL INPORMATION:

APPLICANT: Selsted, Michael E.

APPLICANT: Teat, Dat Q.

TITLE OF INVENTION: Thereof, and Methods of Use

FILE REFERENCE: 66778-302(UC5754)

CURRENT APPLICATION NUMBER: US 510/427,715

CURRENT APPLICATION NUMBER: US 60/377,071

PRIOR APPLICATION NUMBER: US 60/377,071

PRIOR FILING DATE: 2002-04-30

NUMBER OF SEQ ID NOS: 41

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 101; DB 15;
Pred. No. 4.9e-05;
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Pred. No. 4.9e-05;
1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: synthetic construct US-10-427-715-24
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88.9%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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Best Local Similarity 88.9 Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 87.1
Best Local Similarity 83.3
Matches 15, Conservative
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US-10-721-839-30
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TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use
FILE REPERENCE: 65778-302 (UG5754)
CURRENT APPLICATION NUMBER: US/10/427,715
CURRENT PILING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: US 60/377,071
PRIOR PILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

87.1%; Score 101; DB 15; Length 18;
Best Local Similarity 83.3%; Pred. No. 4.9e-05;
Matches 15; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 87.1%; Score 101; DB 15; Length 18; Best Local Similarity 83.3%; Pred. No. 4.9e-05; Matches 15; Conservative 1; Mismatches 2; Indels
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LOCATION: 18
COTHER INFORMATION: at the C terminus
US-10-427-715-13
                                                                                                   Sequence 12, Application US/10427715
Publication No. US20040014669A1
GENERAL INFORMATION:
APPLICANT: Seleted, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GFCRCLCRRGVCRCICTR 18
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  1 GFCRCLCRRGVCRCICTR 18
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US-10-427-715-13
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                                                                                  US-10-427-715-12
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LENGTH: 18
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NS-101-427-715-29

Sequence 29, Application US/10427715

Publication Wo. US20040014669A1

GENERAL INFORMATION:
APPLICANT: Seleted, Michael E.
APPLICANT: Tran, Dat Q.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use
FILE REFERENCE: 66778-302 (UCS)54)

CURRENT APPLICATION NUMBER: US/10/427,715

CURRENT PILING DATE: 2002-04-30

NUMBER OF SEQ ID NOS: 41

SOFTWARE: FBSELSEQ for Windows Version 4.0

SEQ ID NO 29

LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: synthetic construct US-10-427-715-29
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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0; Gaps 1; Indels Query Match

86.2%; Score 100; DB 15;
Best Local Similarity 93.8%; Pred. No. 6.4e-05;
Matches 15; Conservative 0; Mismatches 1; 1 GFCRCICTRGFCRCIC 16

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1 GICRCICTRGFCRCIC 16

ð d US-10-141-645-5

Sequence 5, Application US/10141645

BUBLICARION O. US20030144184A1

GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Alexander Cole
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Autimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: 05/06/06/06
PRIOR FILING DATE: 2002-05-06
PRIOR FILING DATE: 2001-04-18
FRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PastSEQ for Windows Version 4.0

LENGTH: 18

FEATURE:
; OTHER INFORMATION: synthetic variant US-10-141-645-5 TYPE: PRT ORGANISM: Artificial Sequence

80.2%; Score 93; DB 14; Length 18; 77.8%; Pred. No. 0.00039; Indels 1; Mismatches Query Match 80.2 Best Local Similarity 77.8 Matches 14; Conservative

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Gaps

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1 GFCRCICTRGFCRCICTR 18

Search completed: April 28, 2005, 14:26:50

Job time : 91.5 secs

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- 2005 Compugen Ltd.
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April 28, 2005, 14:00:51 ; Search time 26 Seconds (without alignments) 66.612 Million cell updates/sec Run on:

US-10-009-317A-32 116 1 GFCRCICTRGFCRCICTR 18 Perfect score:

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		a			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
1	87	75.0	18	. 7	C59089	theta defensin-1 -
7	64	55.2	76	7	A59089	theta defensin la
3	54.5	47.0	248	7	E71602	ra
4	54	46.6	290	7		AcOrf-70 protein -
S	53	45.7	164	7	T24272	hypothetical prote
9	53	45.7	188	7	T15651	hypothetical prote
7	52.5	45.3	73	7	JC1066	മ
80	51	44.0	72	7	TIMB	
6	51	44.0	419	7	869207	vascular endotheli
10	50.5	43.5	83	~	S07405	proteinase inhibit
11	50.5	43.5	94	7	JC2225	Bowman-Birk protei
12	50.5	43.5	103	٦	TISYC2	ĕ
13	20	43.1	624	Н	S54581	probable membrane
14	49	42.2	152	~	T18975	hypothetical prote
15	49	42.2	157	~	A25964	_
16	49	42.2	1700	7	S08167	Balbiani ring 3 pr
17	48	41.4	72	-1	TIZB1P	겵
18	48	41.4	78	H	TIZBIA	proteinase inhibit
	48	41.4	79	Ч	TIFB2	proteinase inhibit
	48	41.4	83	7	S07941	proteinase inhibit
21	48	41.4	102	٦	TISYD2	proteinase inhibit
	48	41.4	160	7	T25185	hypothetical prote
23	48	41.4	306	7	S32834	
24	48	41.4	476	7	JC5042	G protein-coupled
	48	41.4	1353	H	JH0675	restrictin precurs
26	•	40.9	77	~	I48725	Q300 protein - mou
	47.5	40.9	550	N	PQ0618	hypothetical prote
28	47	40.5	113	~	S56648 ·	д
29	47	40.5	317	~	JC7597	chondromodulin-I 1

tenomodulin - mous	hypothetical prote	hypothetical prote	hypothetical prote	gp330 protein prec	hypothetical prote	related to mutanas	reelin precursor -	proteinase inhibit	hypothetical prote	hypothetical prote	hypothetical prote	latent transformin	unknown protein, 9	gene serrate prote	EF1 protein - fowl
JC7603	T34264	T15840	T22945	T42737	T33983	T49781	S58870	809415	T17298	T09052	C96719	A57293	G96711	S16148	A31685
~	~	~	N	7	7	7	Ŋ	7	7	7	~	~	~	7	~
317	2195	2946	3191	4660	141	883	3461	146	511	761	792	1251	1307	1408	222
40.5	40.5	40.5	40.5	40.5	40.1	40.1	40.1	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.5
47	47	47	47	47	46.5	46.5	46.5	46	46	46	46	46	46	46	45.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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theta defensin-1 - rhesus macaque
NiAlternate names: RTD-1
CiSpecies Macaca mulatta (rhesus macaque)
C;Species Macaca mulatta (rhesus macaque)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: C59089
R;Tang, Y.O.; Yuan, J.; Osapay, G.; Osapay, K.; Tran, D.; Miller, C.J.; Ouellette, A.J.
Science 286, 498-502, 1999
A;Title: A cyclic antimicrobial peptide produced in primate leukocytes by the ligation of A;Reference number: A59089; MUID:99453140; PMID:10521339
A;Accession: C59089
A;Accession: E59089
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-18 <SEL>
A;Note: this sequence is cyclically permuted by -6 residues from the sequence presented C;Comment: For the two contributing precursor sequences, see PIR:A59089 and PIR:B59089.
C;Keywords: antibacterial; antibiotic; antifungal; leukocyte; protein splicing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;10-18/Region: theta defensin 1b-derived F;1.10-18/Cross-link: cyclopeptide (Arg-Cys) #status experimental F;2-11,4-9,13-18/Disallfide bonds: #status experimental F;9-10/Cross-link: cyclopeptide (Cys-Arg) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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86.7%;
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Best Local Similarity
Matches 13; Conserv
C59089
theta defensin-1
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A59089

theta defensin la precursor - rhesus macaque
C;Species: Macaca mulatta (rhesus macaque)
C;Species: Macaca mulatta (rhesus macaque)
C;Species: Jeoct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: A59089
R;Tang, Y.Q.; Yuan, J.; Osapay, G.; Osapay, K.; Tran, D.; Miller, C.J.; Ouellette, A.J.
Science 286, 498-502, 1999
A;Title: A cyclic antimicrobial peptide produced in primate leukocytes by the ligation A;Reference number: A59089; MUID:99453140; PMID:10521339
A;Accession: A59089
A;Accession: A59089
A;Accession: A59089
A;Accession: A59089
A;Accession: A59089
C;Comment: preliminary
A;Molcule type: mRNA
A;Residues: 1-76 crAN>
A;Cross-references: UNIPROT:P82270; GB:AF191100; NID:g6137227; PIDN:AAF04389.1; PID:g61
C;Superfamily: mammalian defensin
C;Superfamily: mammalian defensin
C;Keywords: antibacterial; antibiotic; antifungal; leukocyte; protein splicing
F;1-20/Domain: signal sequence #status predicted cSIG>

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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24272
Submitted to the EMBL Data Library, October 1995
A;Reference number: Z19867
A;Accession: T24272
A;Accession: Preliminary; translated from GB/EMBL/DDBJ
A;Refectus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-164 vMLD>
A;Residues: 1-164 vMLD>
A;Cross-references: UNIPROT:Q22048; EMBL:Z66499; PIDN:CAA91301.1; GSPDB:GN00020; CESP:Tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-188 <NHA>
A;Cross-references: UNIPROT:Q18238; EMBL:U58760; NID:g1330384; PID:g1330389; PIDN:AAB00
A;Experimental source: strain Bristol N2; clone C27A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                trypsin inhibitor - mung bean (5.5pecies: Vigna radiata (mung bean) (5.5pecies: Vigna; V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Molecule type: DNA
A Readdues: 1-73 cCHBA
C'Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
C'Superfamily: Bowman-Birk proteinase inhibitor
C'Superfamily: Bowman-Birk inhibitor #status predicted <MAT>
F;2-73/Product: trypsin inhibitor #status predicted <MAT>
F;4-40/Domain: Bowman-Birk inhibitor repeat homology <BBI>F;4-66/Domain: Bowman-Birk inhibitor repeat homology <BBI>File-6/Domain: Bowman-Birk inhibitor repeat homology <BBIO>File-6/Domain: Bowman-Birk inhibitor repeat homology <BIO>FILE-6/Domain: Bowman-Birk inhibitor repeat homology <BIO>FILE-6/Domain-Birk inhibitor repeat homology <BIO>FILE-6/Domain-Birk inhibitor Birk inhibitor Birk inhibitor Birk inhibitor Birk inhibitor Birk inhibitor Birk inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein C27A2.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T15651
R;Nhan, M.
submitted to the EMBL Data Library, May 1996
A;Description: The sequence of C. elegans cosmid C27A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 7.6;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 GGCGCCCRPRCCCCRR 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: clone T01B7 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.7%;
50.0%;
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Matches 9, Conserv
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Best Local Similarity
Matches 9; Conserv
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A;Map position: 2
A;Introns: 20/3; 90/2
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A, Map position: 2
A, Introns: 19/3; 91/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable integral membrane protein PFB0950w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Datcession: E71602
C;Accession: E71602
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: E71602
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-248 <GAR>
A;Residues: 1-248 <GAR>
A;Residues: 1-248 <GAR>
A;Cross-references: UNIPROT:096282; GB:AE001428; GB:AE001362; NID:g3845316; PIDN:AAC7197
A;Genetics:
A;Genetics:
A;Genetics:
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C;Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
A;NOTE: dBANA Virus
C;Bacciesion: G72858
R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
Virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A;Accession: G72858
A;Accession: Accession: G72858
A;Accession: G72858
A;Accession: Accession: G72858
A;Accession: G72858
A;Accession: Accession: G72858
A;Accession: G7285
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                            F;21-64/Domain: amino-terminal propeptide #status predicted <PRO>F;74-76/Domain: carboxyl-terminal propeptide #status predicted <CTP>
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46.6%; Score 54; DB 2; Length 290;
Best Local Similarity 40.7%; Pred. No. 7.7;
Matches 11; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                          Length 76;
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60.0%; Pred. No. 6;
iive 1; Mismatches 2;
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                                                                                                                                                                                          Score 64; DB 2;
Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                      1; Mismatches
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                                                                                                                                                                                     Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 RCICTRGFCRLL 76
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Best Local Similarity
Matches 9; Conservat
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A;Residues: 'X',104-120 <JOU2>
A;Residues: 'X',104-120 <JOU2>
R;Lee, J.; Gray, A.; Yuan, J.; Luoh, S.M.; Avraham, H.; Wood, W.I.
submitted to the EMBL Data Library, December 1995
A;Description: Vascular endothelial growth factor related protein (VRP): A ligand and Experence number: 869208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Cross-references: UNIPROT: P01063; EMBL: M20732; NID: 9169944; PIDN: AAA33953.1; PID: 9169.
A, Note: the sequences of codons 8-13 and 14-27 are interchanged in the authors' transla R;Back, J.M.; Kim, S.I.
submitted to the EMBL Data Library, October 1992
A, Description: Nucleotide sequence of a cDNA encoding the soybean Bowman-Birk proteinas A, Reference number: $29959
A, Accession: $29608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Glycine max (soybean)
C;Species: Glycine max (soybean)
C;Date: O.2-Dec-1993 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S07405; S29608; S40113
R;Joudrier, P.E.; Foard, D.E.; Floener, L.A.; Larkins, B.A.
R;Joudrier, P.E.; Foard, D.E.; Floener, L.A.; Larkins, B.A.
A;Title: Isolation and sequence of cDNA encoding the soybean protease inhibitors PI IV
A;Reference number: S07405
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C;Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GDB:3890883; OMIM:601528
F;1-12/Domain: signal sequence #status predicted <SIG>
F;13-102/Domain: propeptide #status predicted <PRO>
F;103-419/Product: vascular endothelial growth factor C #status experimental <MAT>
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A;Molecule type: mRNA
A;Residues: 1-83 <BAE>
A;Residues: 1-83 <BAE>
A;Cross-references: EMBL:X68705; NID:g18567; PIDN:CAA48656.1; PID:g18568
A;Cross-references: EMBL:X68705; NID:g18567; PIDN:CAA48656.1; PID:g18568
B;Giordano, A.; Delledonne, M.; Fogher, C.; Marchetti, S.
submitted to the EMBL Data Library, December 1993
A;Description: Nucleotide sequence encoding a soybean C-II proteinase inhibitor.
                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-419 <LEE>
A;Cross-references: EMBL:U43142; NID:g1150988; PIDN:AAAA85214.1; PID:g1150989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Accession: G02659
A,Status: preliminary: translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-419 < wOR>
A,Residues: 1-419 < wOR>
A,Residues: EMBL:U58111; NID:g1373426; PIDN:AAB02909.1; PID:g1373427
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Pred. No. 22;
2; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                      R;Morris, J.C.
submitted to the EMBL Data Library, May 1996
A;Reference number: H01557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 36.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reference number: S40113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
A;Gene: GDB:VEGFC; VRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-83 <JOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-83 <GIO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
                                                                                                                                                                                                                                           A; Accession: S69208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: S07405
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A; Molecule type: protein
A; Residues: 1.72 C-2HA>
A; Residues: 1.72 C-2HA>
A; Cross-references: UNIPROT:P01062
A; Note: three isoinhibitors are also found whose amino ends differ slightly from that sh divs-1, respectively
C; Comment: This inhibitor stoichiometrically inhibits trypsin in a molar ratio of 1:2.
C; Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology C; Keywords: duplication; serine proteinase inhibitor
C; Superfamily: Bowman-Birk inhibitor repeat homology < BB1>
F; 13-39/Domain: Bowman-Birk inhibitor repeat homology < BB2>
F; 12-66, 13-28, 16-62, 18-26, 36-43, 40-55, 45-53/Disulfide bonds: #status predicted
F; 20/Inhibitory site: Lys (trypsin) #status predicted
F; 47/Inhibitory site: Arg (trypsin) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-419 <-JOU>
A; Cross-references: UNIPROT: P49767; EMBL: X34216; NID: g1177488; PIDN: CAA63907.1; PID: e221
A; Cross-references: UNIPROT: P49767; EMBL: X34216; NID: g1177488; PIDN: CAA63907.1; PID: e221
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
A; Note: only a part of the translation is shown
A; Note: this is a revision to the sequence from reference S61795
R; Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksela, A; Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4 (VA; Réference number: S61795; MUID: 96178224; PMID: 8617204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vascular endothelial growth factor C precursor - human
NiAlternate names: FLT4 ligand DHM
C;Bate: 27-Apr. 1996 #sequence revision 01-Nov-1996 #text_change 09-Jul-2004
C;Bate: 27-Apr. 1996 #sequence revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: S69207; S61795; S71443; S69208; G02659
S;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksela, A;Julle: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand fc
A;Reference number: S69207; MUID: 96203094; PMID: 8612600
A;Accession: S69207
A;Accession: S69207
A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Vigna radiata (mung bean)
Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: A01301
R;Zhang, Y.; Luo, S.; Tan, F.; Qi, Z.; Xu, L.; Zhang, A.
Sci. Sin. 25, 268-277, 1982
A;Title: Complete amino acid sequence of mung bean trypsin inhibitor.
A;Reference number: A01301
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                                                  Length 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match
Local Similarity 57.9%; Pred. No. 6.8;
hes 11; Conservative 2; Mismatches 2: TnAmle
                                                                                                                           Indels
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A,Residues: 70-419 <JOUI>
A;Note: this sequence has been revised in reference S69207
A;Accession: S71443
                                                      5;
                                              Score 52.5; DB
Pred. No. 4.6;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        trypsin inhibitor (Bowman-Birk) - mung bean
                                                                                                                                                                                                 3 CR-CICTR---GFCRCI----CTR 18
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40 CKSCICTRSMPGKCRCLDT 58
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                                              45.3%;
                                              Query Match
Best Local Similarity 48.0
Matches 12, Conservative
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Matches
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Gaps

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us-10-009-317a-32.rpr

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EMBL: Z49702; NID: 9817859; PID: 91326013; GSPDB: GN000
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A;Residues: 345-624 <LYE>
A;Cross-references: EMBL:Z49273; NID:g809577; PID:g809578; GSPDB:GN00013; MIPS:YMR119w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable membrane protein YMR119w - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein YM8564.01; hypothetical protein YM9718.18
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S54881; S54488
R;Hunt, S:, Bowman, S.
Submitted to the EMBL Data Library, May 1995
A;Reference number: S54510
A;Reference number: S54510
A;Reference number: S4510
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                                                                                                                                                                                                                                                                                                                                                                1;
F;42-68/Domain: Bowman-Birk inhibitor repeat homology <BB1>
F;69-94/Domain: Bowman-Birk inhibitor repeat homology <BB2>
F;41-95,42-57,45-91,47-55,65-72,69-84,74-82/Disulfide bonds: #status predicted
F;49/Inhibitory site: Ala (elastase) #status predicted
F;76/Inhibitory site: Arg (trypsin) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein C06Al.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18975
R;McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                        Length 103;
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                                                                                                                                                                                                                                                                                                                                                           3; Indels
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F;82-98/Domain: transmembrane #status predicted <TM1>
F;120-136/Domain: transmembrane #status predicted <TM2>
F;211-237/Domain: transmembrane #status predicted <TM3>
F;237-253/Domain: transmembrane #status predicted <TM3>
F;278-294/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                        DB 1;
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                                                                                                                                                                                                                                                                        ; Score 50.5; DB; Pred. No. 10; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 13R
C;Superfamily: probable membrane protein YMR119W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, June 1995 A;Reference number: Z19054 A;Accession: T18975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Cross references: UNIPROT:P54074; EMBL:Z497
A; Experimental source: strain AB972
R; Lye, G.; Churcher, C.M.
submitted to the EMBL Data Library, May 1995
A; Reference number: S54014
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                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 58.8%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rybaek, J.M.; Song, J.C.; Choi, Y.D.; Kim, S.I.
Bloosi. Blootechnol. Bloothem. 58, 843-846, 1994
A.Fitle: Nucleotide sequence homology of 1994
A.Fitle: Nucleotide sequence bomology store in 1994
A.Fitle: Nucleotide sequence bomology series and 1994
A.Fitle: Nucleotide sequence bomology series in 1994
C. Superfamily: Bowman-Birk proteinase inhibitor
C. Superfamily: Bowman-Birk proteinase inhibitor of 11 #status predicted <AMT>
F.19-94/Product: Bowman-Birk inhibitor repeat homology <BB1>
F.30-94/Product: Bowman-Birk inhibitor repeat homology <BB1>
F.60-85/Domain: Bowman-Birk inhibitor repeat homology <BB1>
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C;Species: Glycine max (soybean)
C;Species: Glycine max (soybean)
C;Species: Glycine max (soybean)
C;Accession: A22636; A01302
B;Hammond, R.W.; Foard, D.E.; Larkins, B.A.
B;Hammond, R.W.; Foard, D.E.; Larkins, B.A.
A;Title: Molecular cloning and analysis of a gene coding for the Bowman-Birk protease in A;Reference number: A22489; MUID:84264652; PMID:6086657
A;Contents: annotation
A;Note: the sequence has been revised in reference A92540
B;Hammond, R.W.; Foard, D.E.; Larkins, B.A.
J;Biol. Chem. 260, 7806, 1985
A;Reference number: A92540
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A; Accession: A22636
A; Accession: A22636
A; Residues: 1-103 < CHAM>
A; Rodani, S.; Ikenaka, T.
J. Biochem. 82, 1223-1531, 1977
A; Title: Studies on soybean trypsin inhibitors. XI. Complete amino acid sequence of a sc
A; Reference number: A01302
A; MulD: 78087480; PMID: 599141
A; Residues: 28-103 < ChAM>
A; Residues: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bowman-Birk proteinase isoinhibitor C-II precursor (clone pB24) - soybean C;Species: Glycine max (soybean)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 18-Aug-2000
                                                                                                     Gaps
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                      2; Length 83
                                                                                                         Indels
             43.5%; Score 50.5; DB
58.8%; Pred. No. 8.6;
iive 1; Mismatches
                                                                                                                                                                                        4 RCICTR---GFCRCICT 17
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                                                                                                     10; Conservative
                                                         Best Local Similarity
Matches 10; Conserv
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thyroglobulin - rat (fragments)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Odun-1989 #sequence_revision 30-Jun-1991 #text_change 11-Apr-1997
Ciscossion: A25964
RiMusti, A.M.; Avvedimento, E.V.; Polistina, C.; Ursini, V.M.; Obici, S.; Nitsch, L.; Cc A; Musti, A.M.; Avvedimento, E.V.; Polistina, C.; Ursini, V.M.; Obici, S.; Nitsch, L.; Cc A; Musti, Complete structure of the rat thyroglobulin gene.
A;Reference number: A25964; MUD:86094383; PMID:3455768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-157 <MUS>
A; Cross-references: GB:M1258
A; Cross-references: GB:M1258
A; Note: the authors translated the codon GTG for residue 44 as Leu
C; Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat homol
C; Reywords: dimer; glycoprotein; iodine; thyroid gland; thyroid hormone biosynthesis
F; 35-60/Domain: thyroglobulin type I repeat homology (fragment) <THY1>
F; 35-Modified site: thyroxine (Tyr) #status predicted
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42.2%; Score 49; DB 2; Length 157;
Best Local Similarity 32.0%; Pred. No. 20;
Matches 8; Conservative 4; Mismatches 5; Indels
                                                                                                                                 Query Match
42.2%; Score 49; DB 2; Length 152;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 8; Indels
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A;Gene: CESP:C06A1.6
A;Map position: 2
A;Introns: 22/3
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Search completed: April 28, 2005, 14:22:37 Job time : 28 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 28, 2005, 13:58:25; Search time 114 Seconds

(without alignments)

80.855 Million cell updates/sec
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Title: US-10-009-317A-32
Perfect score: 116
Sequence: 1 GPCRCICTRGFCRCICTR 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 segs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% .
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		tion	macaca mula	mus musculu	mus musculu	mus musculu	mus musculu	oryza sativ	mycobacteri	ciona intes	plasmodium	autographa	neurospora	homo sapien	caenorhabdi	caenorhabdi	caenorhabdi	caenorhabdi	chlamydomon	homo sapien	homo sapien	anopheles g	leishmania	rattus norv	xestia c-ni	anopheles g	drosophila	anopheles g	homo sapien	drosophila	phaseolus a	homo sapien	meriones un
		Description	P82270	Q6p8t4	Q8ch20	094912	Q9d4k2	Q949g1	Q8vj20	09blj1	096282	P41470	Q7seq2	. Q9nrb6	022048	095qy1	018238	017641	Q75nz5	Q75n88	Q75n87	07pj70	094uz6	Q6ry99	Q9pyq3	Q7qbv4	Q8mz55	Q7prp5	Q9ui23	Q6ig37	P01062	Q62q82	Q91zh6
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de	Query	Match	55.2	50.9	50.9	50.9	50.9	50.9	48.7	48.3	47.0	46.6	46.6	46.1	45.7	45.7	45.7	45.7	45.7	45.7	45.7	45.3	45.3	45.3	44.8	44.8	44.8	44.8	44.4	44.0	44.0	44.0	44.0
	Č	Score	64	59	53	59	59	59	56.5	26	54.5	54	54	53.5	53	53			53	53	53	52.5	52.5	52.5		25	52	52	51.5	51	51	51	51
	Result	. i	1	7	e	4	Ŋ	9	7	8	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

9 anopheles g		3 rattus norv	_		3 glycine max	2 arabidopsis	2 glycine soj	8 xylella fas	3 canarypox v	0 brachydanio	4 neurospora		7 caenorhabdi
uvq7Q	P97953	Q91ze3	P49767	Q6aln6	P01063	Q81c9	Q8ru22	Q87b1	Q6v223	Q78xv0	Q781g4	Q9ava3	Q7ywv7
6NV47Q	VEGC MOUSE	Q912 <u>E</u> 3	VEGC. HUMAN	Q6A1N6	IBB2 SOYBN	Q8LC <u>9</u> 2	QBRU22	Q87BL8	Q6V223	Q7SXV0	Q7S1G4	Q9AVA3	Q7YWV7
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336	415	415	419	482	83	91	109	168	222	379	1411	99	212
44.0	44.0	44.0	44.0	44.0	43.5	43.5	43.5	43.5	43.5	43.5	43.5	43.1	43.1
51	51	51	51	51	50.5	50.5	50.5	50.5	50.5	50.5	50.5	20	20
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ALIGNMENTS

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11D TADA MACHU

11D TADA MACHU

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MEDINE-2238257, PubMed=12477932; DOI=10.1073/pnas.242603899;
Attausberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Attschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
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Attschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                              InterPro; IPR002366; Defensin_propep.
Parin; PR00879; Defensin_propep; 1.
PROSITE; PS00269; DEFENSIN; FALSE NEG.
Antibiotic; Defensin; Direct protein sequencing; Pungicide; Signal.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                             Interchain (with C-66 of subunit B)
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                                                                                                                                                                                                                                                                                                                                                                      Score 64; DB 1; Length 76;
Pred. No. 0.34;
1; Mismatches 1; Indels
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Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC061079; AA4161079.1; -.
SEQUENCE 168 AA, 18947 MW; B00FD3D27B9BF768 CRC64;
                                                                                                                                                                                                                                                                                              T -> A (in Ref. 2).
BEA207932A030590 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q6PBT4;
05-JUL-2004 (TrEWBLrel. 27, Created)
05-JUL-2004 (TrEWBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
4931420D14Rik protein.
Name=4931420D14Rik;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                         Potential.
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8242 MW;
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83.3%;
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nes 10; Conservative
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     PIR; A59089; A59089.
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                                                                                                                                                                                                                                                                                                                       76 AA;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CS7BL/6J; TISSUB=Testis;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 12, Last sequence update)
Mus musculus adult.male t22, Last annotation update)
Mus musculus adult.male testis cDNA, RIKEN full-length enriched
library, clone:1700065105 product:hypothetical Cysteine-rich region
Nontaining protein, full insert sequence.
                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
MIXEN FANTOM CONSOrtium;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                            STRAIN=CD-1; TISSUE=Testis;
STRAIN=CD-1; TISSUE=Testis;
Xu X., Bai X., Silvius D., Bscalier D., McFarland L., Xu P.-X.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF465502; AA015675.1; -.
MGD; MGI:1913992; 4931420D14Rik.
SEQUENCE 168 AA; 18957 MW; 8F30D3D27B9BF595 CRC64;
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56.2%; Pred. No. 2.9;
ive 1; Mismatches
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                                                                                                                                                                                                       Basic protein CKT1R3.
Name=4931420D14Rik; Synonyms=Ckt1r3;
                                                                                                                                           Created)
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STRAIN=C57BL/6J; TISSUE=Testis;
The FANTOM Consortium,
81
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Hypothetical
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SEQUENCE FROM N.A.

Adachi J., Alzawa K., Atahira S., Akimura T., Arai A., Aono H.,

A Adachi J., Alzawa K., Atahira S., Pukuda S., Fukunishi Y., Furuno M.,

A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Kato H.,

A Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

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A Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

Sano H., Sasaki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

RA Sogabe Y., Suzuki H., Tamamura T., Yasunishi A., Yoshida K., Yoshino M.,

Muramatsu M., Hayashizaki Y.;

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Testis;

MEDLINE=20530913; Pubmed=11076661; DOI=10.1101/gr.152600;

MEDLINE=20530913; Pubmed=11076661; DOI=10.1101/gr.152600;

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Ronno H., Akiyama J., Nishi K., Kitaunai T., Tashiro H., Itoh M.,

M. Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

M. Yamamoto R., Matsumoto H., Sakaguqhi T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Noneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Namanteu M., Inoue Y., Kira A., Hayashizaki Y.,

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
                                                MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Muramatisation and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=9279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9D4K2 PRELIMINARY; PRT; 173 AA.
Q9D4K2;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OT-2002 (TrEMBLrel. 22, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4931420D14 product:hypothetical Cysteine-rich region Containing protein, full insert sequence.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1913992; 4931420D14Rik.
Hypothetical protein.
SEQUENCE 168 AA; 18931 MW; 7A2BD279612A5E94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.9%; Score 59; DB 2; 56.2%; Pred. No. 2.9;
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
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Best Local Similarity
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Matches
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SEQUENCE FROM N.A.

C STRANN-C57BL/6J; TISSUB=Testis;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayateu N., Hiramoto K., Hiraoka T., Hori F.,
A Mawai J., Kolima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Sakai C., Sakai K.,
A Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
A Sogbe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Buhanatsu M., Hayashizaki Y.,
I Submitted (JUL.2000) Lo the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAINE-2059LL/6J; TISSUE=Testis;
STRAINE-20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE-20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                              the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                           RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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STRAIN=CS7BL/6J; TISSUE=Teetis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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173 AA; 19581 MW; 147B6F155AC29FDF CRC64;
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                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
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Q949G1;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AK016467; BAB30253.1;
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SEQUENCE FROM N.A.
MEDINES-9901743; PubMed=9804551; DOI=10.1126/science.282.5391.1126;
Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind L.,
Koonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pederson J.,
                                                                                                                                                                                                                                                                                                                        Nakayama A., Satou Y., Satoh N.;
"Isolation and characterization of genes that are expressed during Ciona intestinalis metamorphosis.";
Dev. Genes Evol. 211:184-189(2001).
EMBL; AB041857; BAB40596.1; --
HSSP; P00743; ICCF.
                                                                                                                                                                                       Ciona intestinalis.
Eukaryota, Metazoa, Chordata, Urochordata, Ascidiacea, Enterogona,
Phlebobranchia, Cionidae, Ciona.
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Bukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
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GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0004889; F:transembrane receptor activity; IEA.
GO; GO:0007996; P:blood coagulation; IEA.
InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR00181; EGF_2.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR001212; Somatomedin_B.
InterPro; IPR001212; Somatomedin_B.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
101-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein PFB0950w.
                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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PROSITE; PS00010; ASX HYDROXXL; 14.
PROSITE; PS00010; ASX HYDROXXL; 14.
PROSITE; PS01186; EGF_2; 19.
PROSITE; PS01186; EGF_3; 19.
PROSITE; PS01187; EGF_CA; 12.
PROSITE; PS0524; SMB_1; 1.
                                                                                            Created)
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PRINTS; PR00907; THRMBOMODULN.
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58.8%;
                                                                                          (TrEMBLrel. 17,
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                                                      PRELIMINARY;
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Pfam; PF07645; EGF CA;
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                                                                                                                                                                                                                                                      NCBI_TaxID=7719;
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SEQUENCE 937
                                                                                                                                                                         Name=Ci-metal;
                                                                                              01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                       Ci-META1
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                                                                          Q9BLJ1;
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                  RESULT 8
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STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; Pubmed=12218036;
DOI=10.1128/JB.184.19.5479-5490.2002;
Fleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O., Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gape
                                                                                                                                                                                           MEDLINE=21329048; PubMed=11435398; DOI=10.1101/gr.GR-1617R; Mayer K., Murphy G., Tarchini R., Wambutt R., Volckaert G., Pohl T., Duesterhoeft A., Stiekema W., Entian K.D., Terryn N., Lemcke K., Haase D., Hall C.R., van Dodeweerd A.M., Tingey S.V., Mewes H.W., Bancroft I.; "Conservation of microstructure bewtween a sequenced region of the genome of rice and multiple segments of the genome of Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                        Oryza sativa (Rice).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; Liliopsida, Poales, Poaceae;
Ehrhartoidese, Oryzeae, Oryza.
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Pred. No. 5.8;
3; Mismatches 2; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
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163 AA; 18621 MW; BSE62AB951B2AC3C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Hypothetical protein C15ERIPDM.
Name=C15ERIPDM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laboratory strains.";
J. Bacteriol. 184:5479-5490(2002).
EMBL; AE000516; AAK47795.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                       Genome Res. 11:1167-1174(2001).
                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ307662; CAC39030.1; -. Gramene; Q949G1; -. Hypothetical protein. SEQUENCE 274 AA; 28657 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || :||| |:|| :|
137 CRHVCTRSGYCRLVC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 RCCCHRGCCRCRATR 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 CRCICTR-GFCRCIC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 RCICTRGFCRCICTR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 60.00
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
OrderedLocusNames=MT3454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 66.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                         NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MT3454; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical
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                                                                                                                                                                                                                                                                                                                                  thaliana
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Length 290;

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46.6%; Score 54; DB 1;
40.7%; Pred. No. 19;
ive 2; Mismatches
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                                                                                                                        218 FARCFCTNTMQCFCPROGYKCECICRR 244
                                                                                  2 FCRCICT-----RGF-CRCICTR 18
                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AABX01000029; EAA35288.1; -. Interpro; IPR006229; EGF like. PROSITE; PS00022; EGF l; 1. PROSITE; PS01186; EGF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  620 GECSCICRNGFIGENC 635
                                                                                                                                                                                                                                                          26,
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26,
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                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 56.3
                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                            01-MAR-2004 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                          01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              991 AA;
                             Similarity
                                                                                                                                                                                                                                                                                                                 Predicted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=OR74A;
       Query Match
Best Local Simi
Matches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=FGFR3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local 9
                                                                                                                                                                                                                  Q7SEQ2
Q7SEQ2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9NRB6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9NRB6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                               RESULT 11
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                                                                                                                                                                                                     Q7SEQ2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                   MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097; Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Pairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
Shen K., Jing J., Aston C., L'ai Z., Schwartz D.C., Pertea M., Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O., Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C6;
MEDLINE=94303173; PubMed=8030224;
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
"The complete DNA sequence of Autographa californica nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
13.4 Abported and an annotation update)
Hypothetical 34.4 Morein in LEF3-IAP2 intergenic region.
Autographa californica nuclear polyhedrosis virus (AcMMPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 307;
                                                                                                                                                                                                                                                                                                                             fraser C.M., Barrell B.; "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERPRO; IPRO01368, TNFR c6.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 307 AA; 35537 MW; B95A3DB354D4BE71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein. –
SEQUENCE 290 AA; 34408 MW; CA78BA9C8B5AB997 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.0%; Score 54.5; D
60.0%; Pred. No. 18;
tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000519; P_trefoil.
                                                                                                                                                                                                                                                                                                                                                                                    Nature 419:498-511(2002).
EMBL; AE001428; AAC71979.2; -.
PIR; E71602; E71602.
                                                                                                Science 282:1126-1132(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 cscicr---crcics 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polyhedrosis virus.";
Virology 202:586-605(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                      falciparum."
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                                                                                falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Y070_NPVAC

Matches

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A Galagan J.B., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Elkins T., Engels R., Wand D., Nelson M., Washburne M., A Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., A Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., A Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S., Kamal M., Kamwysselis M., Maucell E., Bielke C., Rudd S., Frishman D., Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., A Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B., The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 0:0-0(2003).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neurospora crassa.
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
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56.2%; Pred. No. 55;
.ive 0; Mismatches 7; Indels
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103024 MW; C51719B9F4D54A8E CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mutant fibroblast growth factor receptor 3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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Hypothetical protein C04G6.10.
Name=C04G6.10; ORFNames=C04G6.10;
Caenorhabditis elegans.
Elkaryota; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.7%; Score 53; DB 2; Length 166; 50.0%; Pred. No. 16; 1.1ve 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WormBase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; U55854; AAK68158.1; -.
HSSP; P10969; 1WGT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Bristol N2;
Anderson K., Chissoe S.;
"The sequence of C. elegans cosmid C04G6.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Bristol N2;
Wilson R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston R.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PSO10198; PERSEDENTIN; UNKNOWN 1.
PROSITE; PS010269; DEFENSIN; UNKNOWN 1.
PROSITE; PS01029; EGF 1; UNKNOWN 1.
PROSITE; PS01208; WHFC_1; UNKNOWN 1.
Hypochetical protein.
SEQUENCE 166 AA; 16971 MW; 9D9D130351BB50F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q18238;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein C27A2.5.
Name-C27A2.5; ORFNames=C27A2.5;
                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WormPep; C04G6.10; CE27649.
InterPro; IPR001450; 4Fe4S ferredoxin.
InterPro; IPR006081; DefenSin_alpha.
InterPro; IPR006209; EGF like.
InterPro; IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WormBase; WBGene00015458; C04G6.10.
                                                                                                                                                                                                                                                                                                                                                       STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
WormBase Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GFCRCICTRGFCRCICTR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCGCCCRPRCCCCCRR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                      Chesi M., Brents L.A., Ely S.A., Bais C., Mesri E.A., Robbiani D., Kuchl W.M., Bergsagel P.L.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF238374; AAF97149.1; -. GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                 3,
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                                                                                                                                                                                                                                                                        DB 2; Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MormBep; T01B7.8; CE03592.

MormPep; T01B7.8; CE03592.

MormPep; T01B7.8; CE03592.

InterPro; IPR0016509; GFE_like.

InterPro; IPR006091; Defensin_alpha.

InterPro; IPR006209; EGF_like.

InterPro; IPR001007; VWF^C.

PROSITE; PS00269; DEFENSIN; UNKNOWN_1.

PROSITE; PS00269; DEFENSIN; UNKNOWN_1.

PROSITE; PS01208; VWFC_1; UNKNOWN_1.

PROSITE; PS01208; VWFC_1; UNKNOWN_1.

PROSITE: L64 AA; 16499 MW; C002D48D36C9FCED CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sims M.A.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; Z66499; CAA91301.1; -.
PIR; T24272; T24272.
HSSP; P10969; IKYV.
IntAct; Q22048; -.
                                                                                                                                                                                                                   174 AA; 17810 MW; BC9917E34470B9EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
1-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein T01B7.8.
ORFNames=T01B7.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 AA.
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47.1%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                 2; Mismatches
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MEDLINE=99069613; PubMed=9851916;
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75 GLCVCVCV---CVCVCT 88
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Science 282:2012-2018(1998)
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Matches 8; Conservative
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Best Local Similarity
Matches 9; Conserv
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Q22048
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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R GO; GO:0005576; C:extracellular; IEA.

GO; GO:000652; P:defense response; IEA.

GO; GO:000692; P:defense response; IEA.

R InterPro; IPR001450; 4Fe4S_ferredoxin.

R InterPro; IPR001007; VWF C.

R PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.

R PROSITE; PS00208; UNFC_1; UNKNOWN_1.

R PROSITE; PS01208; VWFC_1; UNKNOWN_1.

R PROSITE; PS01208; VWFC_1; UNKNOWN_1.

R PROSITE; PS01208; WRC_1; UNKNOWN_1.
                                                                             SEQUENCE FROM N.A.
STRAIM-BAISEON N2,
MEDLINE-99069613; PubMed-9851916;
WormBase Consortium;
"Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
45.7%; Score 53; DB 2; Length 188;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 9; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Bristol N2;
Wormbase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; US8760; AAK31463.1; -
PIR; T15651; T15651.
HSSP: P10968; 2CWG.
                                                                                                                                                                                                                                                     "The sequence of C. elegans cosmid C27A2."; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                 Waterston R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-Bristol N2;
Wilson R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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STRAIN=Bristol N2;
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                                                  NCBI TaxID=6239;
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Search completed: April 28, 2005, 14:21:41 Job time : 119 secs

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version 5.1.6 - 2005 Compugen Ltd.

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- protein search, using sw model

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Total number of hits satisfying chosen parameters:

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Post-processing:

Database

Geneseq_16Dec04:*
geneseqp1980s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2001s:*

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:*

2105692 segs, 386760381 residues

Gapop 10.0 , Gapext 0.5

US-10-009-317A-33

Perfect score:

Sequence:

Scoring table:

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12Y retro
111Y retr
Human ret
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Theta def
Anti-vira
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Theta defensin; antimicrobial; cyclic; bacterium; fungus; protozoan; virus; helminth; disinfectant; food preservative; analogue.
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bacteria, yeast, fungi, protozoa and viruses.
                                Ade33803
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Pred. No. 9.6e-06;
Mismatches 0;
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AD008177
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Best Local Similarity 100.
Matches 18; Conservative
     (REGC ) UNIV CALIFORNIA
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WO200068265-A1.
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  AAB35047;
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                                                                                                                                                                                          April 28, 2005, 13:57:35 ; Search time 122.5 Seconds (without alignments) 56.830 Million cell updates/sec
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Abp53299 H
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AD035239 AD035256 AD035263 AAB35037

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ADN08176 ABP53299 AAE33804

AD035241 AD035243 ABP53298 AAB35030

ABP53296 AD035231 AD035242

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Query Match Length

Result Š. ABP53297 AAE33866 ADD95202 ADD35357

ADG70012 ADO35229 ADO35238

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The present invention describes a method (M1) of using a first anti-viral peptide (I) comprising a theta-defensin peptide in an amphipathic alphabalical structure in a lipid environment for reducing the infectivity of a virus. (I) can have viruide and anti-HIV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of anti-viral resistance. (I) can be used for inhibiting the growth and proliferation of a virus and so can be used for; (a) protecting or creating subject from a viral infection, reventing recurrent viral infection in a subject harbouring a latent virus, controlling virus shed from a VS. reducing virus or infection in a contaminated tissue or fluid sample safe for use, or reducing the number of infectious virus particles in a population of viruses. (M1) is useful for reducing the infectivity of a virus; and (c) rendering virus contaminated tissue or fluid sample safe for use, or reducing the number of infections virus particles in a population of viruses. (M1) is useful for reducing the infectivity of a virus in sheep, cattle, horses, swine, cats, fowl and humans e.g. an enveloped virus infecting humans such as chuman immunodeficiency virus (HIV). Preferably, the anti-viral peptide is administered to a patient who is immunosuppressed or to a subject who is a contaminated reducing the virus, where the first anti-viral peptide is most preferably administered to a subject who is a subject or subject in the anti-viral peptide is most preferably administered to a subject who is a subject or subject who is a subject or subject or subject which anti-viral peptide is most preferably administered to a subject who is a subject or subject which are contaminated in the virus contacting the subject or subject which is subject which in the virus contacting the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is chronically, latently or acutely infected with the virus. The present sequence represents a rhesus monkey theta defensin anti-viral peptide, which is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                               amphipathic alpha-helical structure, virucide, anti-HIV; immunisation, viral growth inhibitor; viral proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roller R, Mccray PB, Tack B;
                                                                                                                                                                                                                                                    Anti-viral; viral infection; theta-defensin; lipid environment;
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                                                                                                                                                                                                      Anti-viral theta defensin peptide RTD-3 SEQ ID NO:29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stinski M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 10; 65pp; English.
                                                ABP53296 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JAN-2002; 2002WO-US002435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001; 2001US-0265270P.
01-AUG-2001; 2001US-0309368P.
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                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stapleton J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-674815/72.
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200260468-A2.
                                                                                                                                                                                                                                                                                                                                                             Macaca mulatta
                                                                                                                                                   13-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                                                                                                   ABP53296;
RESULT 2
                          ABP53296
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Monkey, Rhesus theta defensin, RTD-3, antimicrobial peptide, cyclic, antimicrobial; antinflammatory, antibacterial; virucide; fungicide; food, context lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; .18
 Thote="The peptide is cyclised by a covalent link between these two residues"
 fungal infection; haemolytic activity Rhesus theta defensin peptide, RTD-3. Location/Qualifiers Ą. ADO35231 standard; peptide; 18 GVCRCLCRRGVCRCLCRR 18 30-APR-2003; 2003US-00427715. 30-APR-2002; 2002US-0377071P. (first entry) (REGC) UNIV CALIFORNIA. Selsted ME, Tran DQ; WPI; 2004-167945/16. Disulfide-bond Disulfide-bond Disulfide-bond US2004014669-A1 Macaca mulatta Key Modified-site 22-JAN-2004. 15-JUL-2004 AD035231; RESULT 3 AD03523 셤

growth or food Novel theta defensin analog useful for reducing or inhibiting growt survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate object.

Example 1; SEQ ID NO 3; 46pp; English.

The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO35257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism and is useful for reducing or inhibiting to survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism and is useful for reducing or inhibiting growth or survival of a microorganism and is useful for reducing or inhibiting contact. The peptides are also useful for decreasing inflammatory response and for microbistatic inhibition of survival of microorganism as well as microbistatic inhibition of survival of microorganism as well as the peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents the rhesus monkey wild-type theta defensin RTD-3.

Sequence 18 AA;

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Gaps

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Indels

Mismatches

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Conservative

Score 112; DB 8; Length 18; Pred. No. 9.6e-06; 100.0%; 100.0%; Query Match Best Local Similarity

1 GVCRCLCRRGVCRCLCRR 18

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Gaps

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Length 18; Indels

Score 112; DB 8; Pred. No. 9.6e-06; Mismatches

100.0%;

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Conservative

Query Match Best Local Similarity Matches 18; Conserv

18 18

GVCRCLCRRGVCRCLCRR 1 GVCRCLCRRGVCRCLCRR

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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO3527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or growth or survival of a microorganism in an environment such as food or old product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.
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                                                                                                                                                                                                                                                                                   Monkey; Rhesus theta defensin; RTD; antimicrobial peptide; antimicrobial; antiinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection; haemolytic activity.
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   Gaps
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 0; Indels
                                                                                                                                                                                                                                                     Rhesus theta defensin analogue peptide aRTD-3-NH.
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                 ADO35242 standard; peptide; 18 AA
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                                 1 GVCRCLCRRGVCRCLCRR 18
                                                    GVCRCLCRRGVCRCLCRR 18
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Conservative
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Disulfide-bond
Disulfide-bond
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18;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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Matches
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Sequence 18 AA;

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Monkey, Rhesus theta defensin, RTD; antimicrobial peptide; antimicrobial; antiinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; hiflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO35257. The theta defensin analogue is useful for reducing or inhibiting growth or survival
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The thete defensins have high antimicrobial activity and low haemolytic activity. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                                                                                                                                                       Rhesus theta defensin analogue peptide aRTD-3-OH.
                                                                                                                                                                                                                                                                                           fungal infection; haemolytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "Hydroxylated"
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                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                  ADO35241 standard; peptide; 18
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                                                                                                                (first entry)
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Disulfide-bond
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Modified-site
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                                                                         AD035241;
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                AD03524
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Gaps

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The present invention describes a method (M1) of using a first anti-viral peptide (I) comprising a theta-defensin peptide in an amphipathic alphace peptide (I) comprising a theta-defensin peptide in an amphipathic alphace helical structure in a lipid emvironment for reducing the infectivity of a virus. (I) can have virus and anti-H1V activities, and can be used to reduce virus growth, infectivity burden, shed, and development of anti-viral resistance. (I) can be used for inhibiting the growth and proliferation of a virus and so can be used for: (a) protecting or treating subject from a viral infection, preventing recurrent viral crimection in a subject harbouring a latent virus, controlling virus spread within a virally-infected subject (VS) reducing virus latent virus controlling virus shed from a VS, reducing percentege of VS in a copulation regardless of viral infection status, or inducing latency in a volification virus particles in a virus; and (C) rendering the number contaminated tissue or fluid sample safe for use, or reducing the number of infectious virus particles in a population of viruses. (M1) is useful for reducing the infectivity of a virus; in sheep, cattle, horses, swine, cats, fowl and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-viral; viral infection; theta-defensin; lipid environment; amphipathic alpha-helical structure; virucide; anti-HIV; immunisation; viral growth inhibitor; viral proliferation inhibitor.
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peptides are also useful for treating a patient suffering from peptides are also useful for treating a patient suffering from
                                         bactērial, viral, fungal or other infection. The theta defensins have
high antimicrobial activity and low haemolytic activity. The present
sequence represents a Rhesus theta defensin analogue peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-viral chimeric theta defensin peptide H/RTD-3 SEQ ID NO:31.
                                                                                                                                                                                           95.5%; Score 107; DB 8; Length 18; 100.0%; Pred. No. 3.3e-05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 10; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP53298 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                               1 GVCRCLCRRGVCRCLCR 17
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01-AUG-2001; 2001US-0309368P.
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Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                               Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monkey, Rhesus theta defensin, RTD; antimicrobial peptide; antimicrobial; antiinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection; haemolytic activity.
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                                                                                                                                                                           Gaps
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                         sequence represents a Rhesus theta defensin analogue peptide.
                                                                                                                           Length 18;
                                                                                                                                                                           Indels
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                                                                                                                        Score 112; DB 8;
Pred. No. 9.6e-06;
                                                                                                                                                                           Mismatches
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                                                                                                                           100.0%;
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                                                                                                                                                                              Conservative
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                                                                                                                   Query Match
Best Local Similarity
Matches 18; Conserv
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Disulfide-bond
Disulfide-bond
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Modified-site

Synthetic.

22-JAN-2004.

Selsted ME,

object.

15-JUL-2004

AD035243;

RESULT 6

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Tack B;

Mccray PB,

18

8888888888888

8 g

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ABP53297 standard; peptide; 18 AA
ABP53297
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administered to a patient who is immunosuppressed or to a subject who is not infected with the virus, where the first anti-viral peptide is administered prior to or subsequent to the virus contacting the subject. The anti-viral peptide is most preferably administered to a subject who is chronically, latently infected with the virus. The present sequence represents a chimeric human/rhesus monkey theta defensin anti-viral peptide, which is given in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lefensin; antimicrobial; cyclic; bacterium; fungus; protozoan; helminth; disinfectant; food preservative; analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel theta defensin peptide with antimicrobial activity against
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l. .18
'note= "peptide bond cyclises the molecule"
                                                                                                                                                                                                                                                                                                 Length 18;
                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                            Score 102; DB 5;
Pred. No. 0.00012;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bacteria, yeast, fungi, protozoa and viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouellette AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ź
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                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                        18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB35030 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                   Yuan J,
                                                                                                                                                                                                                                                                                               91.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAY-2000; 2000WO-US012842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-00309487
                                                                                                                                                                                                                                                                                                                                                                                                        GVCRCLCRRGVCRCLCRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Theta defensin SEQ ID NO: 1.
                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 83.3-
Best Local Similarity 83.3-
The state of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . . . 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-031853/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Theta defensin;
                                                                                                                                                                                                                                          Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200068265-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-links
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Selsted ME,
                                                                                                                                                                                         invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB35030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB35030
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the peptide (I) comprising a merinou (MI) or using a lifter anti-viral peptide (I) comprising a theta-defensin peptide in an amphipathic alphaelal structure in a lipid environment for reducing the infectivity of a virus. (I) can have virucide and anti-HIV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of anti-viral resistance. (I) can be used for inhibiting the growth and correction of a virus and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling virus spread within a virally-infected subject (VS) reducing virus burden in a VS, reducing virus shed from a VS, reducing virus burden in a VS, (b) reducing virus shed from a VS, reducing virus latent virus, controlling virus contaminated tissue or fluid sample safe for use, or reducing the number of infections virus particles in a population of viruses. (MI) is useful for reducing the infectivity of a virus in sheep, cattle, horses, swine, cats, fowl and humans e.g. an enveloped virus infecting humans such as duministered to a patient who is immunosuppressed or to a subject who is continued to the virus, where the first anti-viral peptide is administered prior to or subsequent to the virus contacting the subject. The anti-viral peptide is an enveloped in contacting the subject who is contacting the virus. The present contacting the subject who is contacting to a subject who is contacting 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention describes a method (M1) of using a first anti-viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ically, latently or acutely infected with the virus. The present represents a rhesus monkey theta defensin anti-viral peptide,
                                                                                                                                                                                                                                                                                    Anti-viral; viral infection; theta-defensin; lipid environment; amphipathic alpha-helical structure; virucide; anti-HIV; immunisation; viral growth inhibitor; viral proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mccray PB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 99; DB 5; Length 18;
Pred. No. 0.00024;
1; Mismatches 2; Indels
                                                                                                                                                                                     Anti-viral theta defensin peptide RTD-1 SEQ ID NO:30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roller R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stinski M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 10; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-2002; 2002WO-US002435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2001; 2001US-0265270P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IOWA ) UNIV IOWA RES FOUND.
                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 88.4
Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maury W, Stapleton J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-674815/72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca mulatta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200260468-A2.
                                                                                          13-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
ABP53297;
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Conservative

Local Similarity nes 15; Conserv

Matches

Query Match

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ö

Gaps

. 0

2; Indels

1; Mismatches

Score 99; DB 4; Length 18; Pred. No. 0.00024;

88.4%;

1. .18
/note= "Residue 1 and residue 18 bond to form a cyclic

Location/Qualifiers

8

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New conjugate of transport mediator and active agent, useful for treating prokaryotic infections, especially by neutralizing antibiotic resistance
                  bacterial infection; human pathogen; holin; defensin; peptide nucleic acid; PNA; penicillin; tetracycline; ampicillin; kanamycin; antibiotic; antibacterial; antibiotic-resistance gene; cyclic.
                                                                                                                                                                                                                                                                                                                   Braun K, Braun I, Debus J, Pipkorn R,
                                                                                                                                                                                                                                                                                          DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 10; 34pp; German.
                                                                                                                                                                                                                                                                    18-JAN-2002; 2002DE-01001862.
                                                                                                                                                                                                                                            17-JAN-2003; 2003WO-DE000124
Cyclic defensin fragment.
                                                                                                                               moiety"
3. .16
5. .14
7. .12
                                                                                                                                                                                                                                                                                                                                        WPI; 2003-689464/65
                                                                                              Key
Misc-difference
                                                                                                                                            Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                             WO2003059392-A2
                                                                      Unidentified
                                                                                                                                                                                                                    24-JUL-2003.
                                                                                                                                                                                                                                                                                            (DEKR-)
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections act as a such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is rheaus monkey theta defensin, RIDI peptide. This sequence is used in the exemplification of the invention
                                                                                                                                                                                            Retrocyclin, infection, sexually transmitted disease, gene therapy, HIV, human immunodeficiency virus; bacterial vaginosis; ophthalmic infection, antibiotic modelling; antimicrobial; rhesus monkey; theta defensin 1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually
                                                                                                                                                                                                                                                                                                                                                                                                                                                        isolated retrocyclin peptide, useful for preventing retroviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 99; DB 6; 1
Pred. No. 0.00024;
1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                        ŢB;
                                                                                                                                                                                                                                                                                                                                                                                                        Hong
                                                                                                AAE33866 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Fig 3C; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         Cole AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transmitted diseases, vaginosis.
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             GVCRCLCRRGVCRCLCRR 18
                          GFCRCLCRRGVCRCICTR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.4%;
                                                                                                                                                                                                                                                                                                                                18-APR-2002; 2002WO-US012353.
                                                                                                                                                                                                                                                                                                                                                        18-APR-2001; 2001US-0284855P
                                                                                                                                                                     Macaca mulatta RTD1 peptide
                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 83.3 Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                         Waring AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-103387/09.
                                                                                                                                                                                                                                                         Macaca mulatta.
                                                                                                                                                                                                                                                                                 WO200285401-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18 AA;
                                                                                                                                              16-APR-2003
                                                                                                                                                                                                                                                                                                       31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                      RI,
                                                                                                                        AAE33866;
                                                                                                                                                                                                                                                                                                                                                                                                        Lehrer
                                                                        RESULT
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Waldeck W;

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This invention describes a novel conjugate for treating prokaryotic confections which comprises a transport mediator for passage through the prokaryotic cell membrane and a compound, directed against a prokaryote and intended for introduction into it. The prokaryote is a bacterium, especially one pathogenic in humans. The transport mediator is preferably a human peptide or protein, especially a phage-holin protein, its active fragment or variant or a defensin. The introduced compound is a peptide conclet acid (PNA) that inhibits a gene, especially one implicated in resistance to penicillin, tetracycline, ampicillin or kanamycin. The conjugate has the structure transport mediator-space-rpNA where the spacer is linked to the transport mediator through a cleavable disulfide bridge. The conjugates are administered together with a natibiotic, by parenteral, transdermal or subcutaneous routes. The products of the invention have antibiotics, for treating prokaryotic, especially in combination with antibiotics are administered against the antibiotic-resistance gene. Where the PNA is directed against the antibiotic-resistance gene. Where the PNA is directed against creasistant to at least one antibiotic and then the PNA is directed against the antibiotic resistance gene. Where the PNA is directed against creasistance gene where normally they would be ineffective. This sequence represents a cyclic defensin fragment described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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Pred. No. 0.00024;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GFCRCLCRRGVCRCICTR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVCRCLCRRGVCRCLCRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 83.3
nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 AA;
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RESULT 12

ADD95202 standard; peptide; 18 AA.

RESULT 11 ADD95202 (first entry)

29-JAN-2004

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ADD95202;

18 18

1 GVCRCLCRRGVCRCLCRR GVCRCICTRGFCRCLCRR

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microbial cell-wall biosynthesis; immunomodulation; anticoagulant.
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                                                                                                                                   (FARB ) BAYER HEALTHCARE AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Conservative
                                                                                                                                                          Newton B,
                                                                                                                                                                             WPI; 2004-071500/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                            WO2003105883-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 AA;
                       Macaca mulatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca mulatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
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                                                                  24-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AD035229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                          Ladel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel ophthalmic solution comprising a prostaglandin of the F-series and an antimicrobial peptide. A solution of the invention has hypotensive and ophthalmological activity. The solution is useful for the treatment of increased intraocular pressure, such as caused by glaucoma and for the reduction of ocular hypetension. The prostaglandin and the antimicrobial peptide work synergistically, to provide beneficial reduction in the incidence of irritant and toxic side effects such as hyperaemia, irritation and inflammation of conjunctiva, ocular cell dysplasia, iridial melanocyte hyperplasia, and hyperpigmentation, associated with the prior art prostaglandin compositions. The present sequence represents an antimicrobial peptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rhesus theta defensin-1; RTD-1; bacteraemia; lipopolysaccharide; LPS;
lipteichonic acid; LTA; septic shock; antibacterial; fungicide; virucide;
immunomodulator; anticoagulant activity;
                                                                                               antimicrobial; ophthalmic; prostaglandin; hypotensive; ophthalmological; intraocular pressure; glaucoma; ocular hypertension; hyperaemia; irritation; inflammation; conjunctiva; ocular cell dysplasia; iridial melanocyte hyperplasia; hyperpigmentation.
                                                                                                                                                                                                                                                                                                                                      Ophthalmic solution useful for the treatment of increased intraocular pressure comprises a prostaglandin of the F-series and an antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 99; DB 8; members Pred. No..0.00024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhesus theta-defensin-1 (RTD-1) peptide.
                                                                          Antimicrobial peptide theta-defensin.
                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 11; 11pp; English.
          ADD35357 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADG70012 standard; peptide; 18
                                                                                                                                                                                                                                               21-MAR-2002; 2002US-0367071P.
                                                                                                                                                                                                                         21-MAR-2003; 2003WO-US008935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GVCRCLCRRGVCRCLCRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GFCRCLCRRGVCRCICTR
                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                           Maxey KM, Johnson J;
                                                                                                                                                                                                                                                                     (CAYM-) CAYMAN CHEM
                                                                                                                                                                                                                                                                                                                 WPI; 2004-011506/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                             WO2003079997-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention
                                                     15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAR-2004
                                                                                                                                                                                                 02-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
                                ADD35357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADG70012;
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ADD35357
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for preparing a composition for treatment and/or prevention of bacteraemia for binding bacterial products such as lipopolysaccharide (LPS) and/or lipteichonic acid (LTA), or for treatment and/or prevention of septic shock. RTD-1, isolated from immune cells of rhesus monkeys, has antibacterial, fungicide, virucide, immunomodulator and anticoagulant activity. RTD-1 inhibits microbial cell-wall biosynthesis and also binds to LPS and LTA. RTD-1 for treatment and prevention of severe infections caused by Gram-positive or -negative bacteria and yeasts, or by viruses. RTD-1 combines four advantageous properties: a direct antimicrobial action, neutralisation of bacterial products (by binding),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes the novel use of rhesus theta defensin-1 (RTD-1)
                                                                                                                                                                                                                                                                                                                                                                                                                     Use of rhesus theta defensin-1 for treating or preventing bacteremia and septic shock, also for binding bacterial products and as immunomodulator and anticoagulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunomodulation (reducing release of proinflammatory cytokines but increasing release of regulatory factors) and anticoagulant action, so provides a better and simpler treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monkey, Rhesus theta defensin, RTD-1; antimicrobial peptide; cyclic, antimicrobial; antinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps

    18 'The peptide is cyclised by a covalent link
between these two residues"

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                                                                                                                                                                                                                                                        Gerdes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                        Brunner N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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                                                                                                                                                                                                                                                        Labischinski H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhesus theta defensin peptide, RTD-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; SEQ ID NO 1; 28pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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30-MAY-2003; 2003WO-EP005694.
                                                                                  13-JUN-2002; 2002DE-01026216.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO35257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from sequence represents the rhesus monkey wild-type theta defensing have sign and antimicrobial activity and low haemolytic activity. The present sequence represents the rhesus monkey wild-type theta defensing TD-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monkey, Rhesus theta defensin, RTD, antimicrobial peptide, antimicrobial, antiinflammatory, antibacterial, virucide, fungicide, food, contact lens solution, eye wash solution, inflammatory response; microbicidal inhibition, microbistatic growth inhibition, disinfectant, food preservative, bacterial infection, viral infection, disinfectant, fungal infection, haemolytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                         Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhesus theta defensin analogue peptide aRTD-1-OH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 1; 46pp; English
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                                                                                                                                                                               30-APR-2003; 2003US-00427715
                                                                                                                                                                                                                              30-APR-2002; 2002US-0377071P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-2004 (first entry)
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Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                     Tran DO
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-167945/16.
Disulfide-bond
Disulfide-bond
Disulfide-bond
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Synthetic.
                                                                                                                                     22-JAN-2004.
                                                                                                                                                                                                                                                                                                                     Selsted ME,
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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO3527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for theating a patient suffering from the peptides are also useful for whemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; SEQ ID NO 12; 46pp; English.
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                                                                                                                                                                 /note= "Hydroxylated"
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                            30-APR-2002; 2002US-0377071P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA.
                              3. .16
5. .14
7. .12
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Best Local Similarity
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                                 Disulfide-bond
Disulfide-bond
Disulfide-bond
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 AA;
                                                                                                                                                                                                                                US2004014669-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Selsted ME,
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ORGANISM: Macaca mulatta
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LENGTH: 18
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Sequence 1, Appli
                                                                                                                         April 28, 2005, 14:12:37; Search time 30 Seconds (without alignments) 44:789 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence 9, M
Sequence 1, M
Sequence 3, M
Sequence 4, M
Sequence 6, M
Sequence 7, M
Sequence 7, M
Sequence 9, M
Sequence 9, M
Sequence 22, Sequence 22, Sequence 66, Sequence 66, Sequence 66, Sequence 66, Sequence 66, Sequence 66, Sequence 67, Sequence 67, Sequence 67, Sequence 67, Sequence 67, Sequence 66, Sequence 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1,
Sequence 9,
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Sequence 1
Sequence 2
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-309-487-1
US-09-367-808-1
US-09-367-808-9
US-10-141-645-1
US-10-141-645-2
US-10-141-645-4
US-10-141-645-5
US-10-141-645-5
US-10-141-645-5
US-10-141-645-5
US-09-309-487-22
US-09-309-487-22
US-09-309-487-22
US-10-141-645-6
US-10-141-645-6
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US-09-309-487-16
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-10-141-645-73
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US-09-604-864-1
                                                                                                                                                                                                                                                                                                                                                                               513545 segs, 74649064 residues
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                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                    US-10-009-317A-33
112
1 GVCRCLCRRGVCRCLCRR 18
                                                                                                                                                                                                                                                                                                                                Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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No.
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US-09-967-808-1
; Sequence 1, Application US/09967808
; Sequence 1, Application US/09967808
; Sequence 1, Application US/09967808
; Batent No. 6514727
; GENERAL INFORMATION:
    APPLICANT: Seleted, Michael E.
    APPLICANT: Tang, Yi-Quan
; APPLICANT: Yuan, Jun
APPLICANT: Ouellette, Andre J.
    TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using
    TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using
    TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using
    TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using
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    TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using
    TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using
    TITLE OF INVENTION NUMBER: US/09/309,487
    PRIOR APPLICATION NUMBER: US/09/309,487
    PRIOR FILING DATE: 2001-09-26
    NUMBER OF SEQ ID NOS: 31
    SOFTWARE: Patentin Ver. 2.0
    SEQ ID NO 1
    LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Selsted, Michael E. CIAT
APPLICANT: Tang, Yi-Quan
APPLICANT: Tang, Yi-Quan
APPLICANT: Yan, Jun
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REFERENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT FILING DATE: 1999-05-10
WINMER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                 Sequence 3250, 75 Sequence 40304, A Sequence 5520, A Sequence 13, Appl Sequence 1, Appli Sequence 2, Appli Sequence 4, Appli
                                                                                                              27, Appl
45, Appl
121, App
65, Appl
69, Appl
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Pred. No. 9.3e-06;
1; Mismatches 2; Indele
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US-10-042-872-1

US-09-510-238A-286

US-09-9487-20

US-09-967-808-20

US-10-141-645-45

US-10-141-645-45

US-10-141-645-65

US-10-141-645-69

US-10-141-645-69

US-10-141-645-69

US-10-141-645-69

US-09-252-991A-32502

US-09-270-76-740304

US-09-270-76-75520

US-09-270-76-5520

US-10-141-645-33

US-10-141-645-33

US-10-141-645-33

US-10-141-645-33

US-08-899-811-4

US-08-899-811-4

US-08-999-811-4

US-08-09-105-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-309-487-1; Sequence 1, Application US/09309487; Patent No. 6335318; GENERAL INFORMATION:
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Best Local Similarity 83.3
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.1%; Score 92; DB 4; Length 18; 66.7%; Pred. No. 6e-05;
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patent No. 6713078

GRMERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alexander Cole
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT PLING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/284,855
PRIOR APPLICATION NUMBER: Unassigned
PRIOR APPLICATION NUMBER: Unassigned
RIOR APPLICATION NUMBER: Unassigned
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 18
                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
PRIOR PELICATION NUMBER: 60/284,855
PRIOR PELICATION NUMBER: 60/284,855
PRIOR PELICATION NUMBER: 10nassigned
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOSTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                   ; Sequence 1, Application US/10141645; Patent No. 6713078
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ORGANISM: Artificial Sequence
3 GFCRCLCRRGVCRCIC 18
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Best Local Similarity 66.73
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CRGANISM: Homo sapiens
US-10-141-645-1
                                                                      RESULT 5
US-10-141-645-1
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LENGTH: 18
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APPLICANT: Tangy 'Yi-Quan
APPLICANT: Tangy 'Yi-Quan
APPLICANT: Yuan, Jun
APPLICANT: Yuan, Jun
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REPERBUCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT FILING DAFE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
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US-09-967-808-9

Sequence 9, Application US/09967808

Sequence 9, Application US/09967808

Sequence 9, Application US/09967808

SENERAL INFORMATION:
APPLICANT: Tang, Yi-Quan
APPLICANT: Yuan, Jun
APPLICANT: Yuan, Jun
APPLICANT: Wan, Jun
APPLICANT: Same
FILE REFRENCE: P-UC 3095

TITLE OF INVENTION: Same
FILE REPRENCE: P-UC 3095

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: US/09/967,808

CURRENT FILING DATE: 1999-05-10

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Ver. 2.0

LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

84.8%; Score 95; DB 3; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.7e-05;
Matches 14; Conservative 1; Mismatches 1; Indels
                                                                                                 Length 18;
                                                                                               Query Match 88.4%; Score 99; DB 4; Length 18; Best Local Similarity 83.3%; Pred. No. 9.3e-06; Matches 15; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                          US-09-309-487-9
, Sequence 9, Application US/09309487
, Patent No. 6335318
, GENERAL INFORMATION:
                                                                                                                                                                                                                          1 GFCRCLCRRGVCRCICTR 18
                                                                                                                                                                                              1 GVCRCLCRRGVCRCLCRR 18
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; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-967-808-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Macaca mulatta
US-09-309-487-9
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US-09-967-808-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                   GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Talexander Cole
APPLICANT: Teresa Hong
ITLE OF INVENTION: Retrocyclins - Antiviral and
ITLE OF INVENTION: Antimicrobial Peptides
FILE REPERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 88; DB 4; 1
Pred. No. 0.00018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - Antiviral and
                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 0202-05-06
PRIOR APPLICATION NUMBER: 00/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: Unassigned
PRIOR APPLICATION NUMBER: Unassigned
PRIOR APPLICATION NUMBER: Unassigned
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
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APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: Unassigned
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: synthetic variant US-10-141-645-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COTHER INFORMATION: synthetic variant US-10-141-645-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/10141645; Patent No. 6713078; GENERAL INFORMATION:
APPLICANT: Robert Lehrer
                          ; Sequence 5; Application US/10141645; Patent No. 6713078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GVCRCLCRRGVCRCLCRR 18
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7%;
Matches 12; Conservative
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Best Local Similarity 66.73
Matches 12; Conservative
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LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.5%; Score 89; DB 4; Length 18; 66.7%; Pred. No. 0.00013; tive 3; Mismatches 3; Indels
                                           GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Talexander Cole
APPLICANT: Teresa Hong
ITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT FILING DATE: 2002-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Alban Waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Retrocyclins - Peptides
FILE REPERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT APPLICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 125
NUMBER OF SEQ ID NOS: 125
NUMBER OF SEQ ID NOS: 125
                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: Unassigned
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION: synthetic variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: synthetic variant
Sequence 3, Application US/10141645
Patent No. 6713078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/10141645 Patent No. 6713078
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Best Local Similarity 66.74
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-141-645-3
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LENGTH: 18
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LENGTH: 18
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Score 77; DB 4; Length 10, Pred, No. 0.0033; 4; Indels
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| Sequence 9, Application US/10141645
| Patent No. 6713078
| General Normation:
| APPLICANT: Robert Lehrer
| APPLICANT: Robert Lehrer
| APPLICANT: Alan Waring
| APPLICANT: Alexander Cole
| APPLICANT: Aexander Cole
| APPLICANT: Aexander Cole
| TITLE OF INVENTION: Antimicrobial Peptides
| TITLE OF INVENTION: Antimicrobial Peptides
| FILE REFERENCE: UCLA-001CIP
| CURRENT APPLICATION NUMBER: US/10/141,645
| CURRENT APPLICATION NUMBER: 60/284,855
| PRIOR APPLICATION NUMBER: Unassigned
| PRIOR PILING DATE: 2001-04-18
| PRIOR FILING DATE: 2001-04-18
| NUMBER OF SEQ ID NOS: 125
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO
                                                                                                            Sequence 8, Application US/10141645;
Patent No. 6713078;
GENERAL INFORMATION:
APPLICANT: Robert Lehrer;
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan Waring
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP;
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT APPLICATION NUMBER: 2002-05-06
PRIOR APPLICATION NUMBER: 2002-06-06
PRIOR PILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 125
SEQ ID NOS
SEQ ID NOS: 128

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: synthetic variant US-10-141-645-8
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ORGANISM: Artificial Sequence
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Best Local Similarity 55.6%;
Matches 10; Conservative
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  1 RCICTRGFCRCLCRR 15
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Best Local Similarity 55.69
Matches 10, Conservative
                                                                        RESULT 13
US-10-141-645-8
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Pest Local Similarity 80.0%; Pred. No. 0.0015;
Matches 12; Conservative 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 75.9%; Score 85; DB 4; Length 18; Best Local Similarity 61.1%; Pred. No. 0.00039; Matches 11; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                   APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Antimicrobial Peptides
FILE REPRENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: Unassigned
PRIOR APPLICATION NUMBER: Unassigned
PRIOR PILING DATE: 2002-04-18
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-17-340-53

Sequence 53, Application US/09917340

Patent No. 6696238

GENERAL INFORMATION:
APPLICANT: McAnilty, Christopher J.
APPLICANT: McAnilty, Jonathan F.
TITLE OF INVENTION: Transplant Media
FILE REPERENCE: TPLANT-06468

CURRENT APPLICATION NUMBER: 05/09/917,340

CURRENT FILING DATE: 2001-07-29

PRIOR FILING DATE: 2001-07-28

PRIOR FILING DATE: 2000-11-17

SOFTWARE: PAPLICATION NUMBER: 60/290,932

PRIOR FILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 96

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 53

LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: synthetic variant US-10-141-645-7
                                                                                                                                                   Sequence 7, Application US/10141645
Patent No. 6713078
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US-09-917-340-53
                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                       RESULT 11
US-10-141-645-7
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RESULT 15
US-09-303-487-22
Sequence 22, Application US/09309487
Fatent No. 6335318
SERERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Yang, Yi-Quan
APPLICANT: OHellette, Andre J.
TITLE OF INVENTION: Andre J.
SOFTWARE: Patent IN Ver. 2.0
SEQ ID NO 2.2
TYPE: PRT
ORGANISM: Macaca mulatta
JOSEPH J.
TITLE OF INVENTION: Andre J.
TYPE: PRT
ORGANISM: Macaca mulatta
JOSEPH J.
TYPE: PRT
A RCLCRRGVCRCLCR I?
TYPE: PRT
A RCLCRRGVCRCCR I?
TYPE: PRT
A RCLCRRGVCRCR II
TYPE: PRT
A RCLCRGVCRCR II
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A RCLCRRGVCRCR II
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A RCLCRRGVCRCR II
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 29, Appl	Sequence 3, Appli	15,	Sequence 16, Appl	29,	Sequence 17, Appl	Sequence 31, Appl	31,	30,	Sequence 1, Appli	Sequence 1, Appli	Sequence 12, Appl	Sequence 13, Appl
QI	US-10-060-102-29	US-10-427-715-3	US-10-427-715-15	US-10-427-715-16	US-10-721-839-29	US-10-427-715-17	US-10-060-102-31	US-10-721-839-31	US-10-060-102-30	US-10-313-994-1	US-10-427-715-1	US-10-427-715-12	US-10-427-715-13
DB	14	15	15	15	15	15	14	15	14	14	15	15	15
% Query Match Length DB	18	18	18	18	18	18	18	18	18	18	18	18	18
% Query Match	100.0	100.0	100.0	100.0	100.0	95.5	91.1	91.1	88.4	88.4	88.4	88.4	88.4
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US-1 US-1 US-1 US-1	222222222		15 US-10-427-715-31 5 US-09-917-340-53 17 US-10-844-837-53 17 US-10-909-119-67 14 US-10-141-645-8 15 US-10-427-715-38 15 US-10-427-715-38
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ALIGNMENTS

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SCHERCAL INCOGRAPHICAL AND ACK
APPLICANT: STAPLETON, JACK
APPLICANT: STAPLETON, JACK
APPLICANT: STANLER, RICHARD
APPLICANT: STINSKI, MARK
APPLICANT: STINSKI, MARK
APPLICANT: MCCRAY, PAUL B.
APPLICANT: MCCRAY, PAUL B.
APPLICANT: MCCRAY, PAUL B.
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL.
TITLE OF INVENTION: CATHELICIDINS
FILE REFERENCE: IOWA:035US
CURRENT APPLICATION NUMBER: 60/309,368
FRIOR APPLICATION NUMBER: 60/309,368
FRIOR APPLICATION NUMBER: 60/265,270
FRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PALENTIN VET. 2.1
SEQ ID NO 29
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: Peptide US-10-060-102-29
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100.0%; Score 112; DB 14;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 18; Conservative 0; Mismatches 0;
US-10-060-102-29
i Sequence 29, Application US/10060102
i Publication No. US20030022829A1
i GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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APPLICAMY: Tran, Dat Q.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use
FILE REFERENCE: 6778-302 (U55754)
CURRENT APPLICATION NUMBER: US/10/427,715
CURRENT FILING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: US 60/377,071
PRIOR PILING DATE: 2000-04-30
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 112; DB 15; Best Local Similarity 100.0%; Pred. No. 3.5e-06; Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: at the C terminus US-10-427-715-16
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
APPLICANT: Selsted, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 18; Conserva
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US-10-721-839-29
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                                                                                                                                             Sequence 3, Application US/10427715
Fublication No. US20040014669A1
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tran, Dat Q.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use
TILE REFERENCE: 66778-302 (US5754)
CURRENT APPLICATION NUMBER: US 60/377,715
CURRENT RILING DATE: 2003-04-30
PRIOR PILING DATE: 2003-04-30
PRIOR PILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Mindows Version 4.0
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100.0%; Score 112; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 18; Conservative 0; Mismatches no. 7-2-1
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US-10-427-715-15
is Gaquence 15, Application US/10427715
is Sequence 15, Application US/10427715
is Dublication No. US20040014669A1
is GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Selsted, Michael E.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
FILE REFERENCE: 66778-302 (UC5754)
CURRENT FILING DATE: 2003-04-30
CURRENT FILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PESESEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: synthetic construct US-10-427-715-15
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; Sequence 16, Application US/10427715
; Publication No. US20040014669A1
; GENERAL INFORMATION:
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1 GVCRCLCRRGVCRCLCRR 18
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ORGANISM: Artificial Sequence
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US-10-427-715-3
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LENGTH: 18
TYPE: PRT
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Length 18;

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US-10-/21-839-29

Sequence 29, Application US/10721839

Publication No. US20040086535A1

GENERAL INFORMATION:

APPLICANT: MAURY, WENDY

APPLICANT: STALEEN. NICHARD

APPLICANT: STINSKI, MARK

APPLICANT: STINSKI, MARK

APPLICANT: TACK, BRIAN

TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL

TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL

TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL

TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL

TITLE OF INVENTION NUMBER: US/10/721,839

CURRENT APPLICATION NUMBER: US/10/060,102

FRIOR PRILING DATE: 2001-001

PRIOR PRILING DATE: 2001-01-30

PRIOR PRILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

SEQ ID NO 29

LENGTH: 18

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US-10-721-839-29
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APPLICANT: STAPLETON, JACK
APPLICANT: STAPLETON, JACK
APPLICANT: STAPLETON, JACK
APPLICANT: STAPLETON, JACK
APPLICANT: STANKI, MARK
APPLICANT: ROLLER, MARK
APPLICANT: MCRAY, PAUL B.
APPLICANT: MCRAY, PAUL B.
TITLE OF INVENTION: CATHELICIDINS
TITLE OF INVENTION NUMBER: US/10/66,102
PRIOR PELLING DATE: 2003-01-22
PRIOR PELLING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 31
LENGTH: 18
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Sequence 30, Application US/10060102

APPLICANT: MARNEY

APPLICANT: STAPEGION, JACK

APPLICANT: STINSKI, MARK

APPLICANT: ACCRAY, PAUL B.

TITLE OF INVENTION: CATHELICIDINS

TITLE OF INVENTION: CATHELICIDINS

TITLE OF INVENTION: LOWA: 0.35US

CURRENT APPLICATION NUMBER: US/10/060,102

CURRENT APPLICATION NUMBER: 60/309,368

PRIOR APPLICATION NUMBER: 60/265,270

PRIOR PILING DATE: 2001-08-01

PRIOR PILING DATE: 2001-08-01

PRIOR SEQ ID NOS: 32

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PATENTIN Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Best Local Similarity 83.3%; Pred. No. 4.5e-05;
Matches 15; Conservative 2; Mismatches 1;
                                                                                                                                                                                  ; Sequence 31, Application US/10721839; Publication No. US20040086535A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                              US-10-721-839-31
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LENGTH: 18
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TITLE REPERENCE: IOWA:0350S
CURRENT APPLICATION NUMBER: US/10/060,102
CURRENT FILING DATE: 2002-02-22
PRIOR PAPLICATION NUMBER: 60/309,368
PRIOR PILING DATE: 2001-08-01
PRIOR PILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VOY: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                 Sequence 17, Application US/10427715
Fublication No. US20040014669A1
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tran, Dat Q.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use
FILE REFERENCE: 66778-302 (UG5754)
CURRENT APPLICATION NUMBER: US/10/427,715
FRIOR APPLICATION NUMBER: US 60/377,071
FRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 41
SOUTHWARE: FASTSEQ for Windows Version 4.0
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95.5%; Score 107; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31, Application US/10060102; Publication No. US20030022829A1 GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
APPLICANT: STAPLETON, JACK
APPLICANT: STINSKI, MARK
APPLICANT: STINSKI, MARK
APPLICANT: ATTACK, BRIAN
APPLICANT: TACK, BRIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: AMIDATION
LOCATION: 18
COTATION: 18
US-10-427-715-17
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LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
                                                  -10-427-715-17
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LENGTH: 18
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RESULT 12
US-10-427-715-12

is Sequence 12, Application US/10427715

is Publication No. US20040014669A1

is Publication No. US20040014669A1

is APPLICANT: Selsted, Michael E.

APPLICANT: Tarn, Dat Q.

itTILE OF INVENTION: Antimicrobial Theta Defensins, Analogs

TITLE OF INVENTION: Thereof, and Methods of Use

TITLE OF INVENTION: Thereof, and Methods of Use

CURRENT PILING DATE: 2003-04-30

PRIOR APPLICATION NUMBER: US/10/427,715

PRIOR APPLICATION NUMBER: US 60/377,071

PRIOR APPLICATION NUMBER: US 60/377,071

PRIOR SEQ ID NOS: 41

SOFTWARE: PastSEQ for Windows Version 4.0

IENGTH: 18
15; Conservative
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Best Local Similarity
Matches 15; Conserv
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APPLICANT: Yang, Yi-Quan
APPLICANT: Yang, Jun
APPLICANT: Obellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REFERENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/10/313, 994
CURRENT FILING DATE: 2002-12-05
PRIOR FILING DATE: 1999-05-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                        Gaps
         ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-060-102-30
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Sequence 1, Application US/10427715

Bublication No. US20040014669A1

GENERAL INFORMATION:

APPLICANT: Selsted, Michael E.

TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs

TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs

TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs

FILE REFERENCE: 66778-302 (UC5754)

CURRENT APPLICATION NUMBER: US/10/427,715

CURRENT FILING DATE: 2003-04-30

PRIOR PRILING DATE: 2002-04-30

NUMBER OF SEQ ID NOS: 41

SOFTWARE: FASTERQ for Windows Version 4.0

LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.4%; Score 99; DB 15; Length 18; 83.3%; Pred. No. 9.7e-05; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 99, DB 14; Length 18;
Pred. No. 9.7e-05;
1; Mismatches 2; Indels
                                                                                                                      Score 99; DB 14; Length 18;
Pred. No. 9.7e~05;
                                                                                                                                                                     2; Indels
                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10313994 Publication No. US20030162718A1 GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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Best Local Similarity 83.3%;
Matches 15; Conservative
                                                                                                                      Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
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SOFTWARE: PatentIn Ver. 2.0
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US-10-427-715-1
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Best Local Similarity
Matches 15; Conserva
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US-10-427-715
US-10-427-7
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Local Similarity 83.3%; Pred. No. 9.7e-05;
les 15; Conservative 1; Mismatches 2; Indels
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                                                                                          , OTHER INFORMATION: synthetic construct US-10-427-715-12
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CTHER INFORMATION: at the C terminus US-10-427-715-13
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Search completed: April 28, 2005, 14:26:50 Job time: 91.5 secs
1 GFCRCLCRRGVCRCICTR 18
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Sublication No. US20040086535A1
GENERAL INFORMATION:
APPLICANT: WARRY
APPLICANT: STAPLETON, JACK
APPLICANT: STAPLETON, JACK
APPLICANT: STINSKI, MARK
APPLICANT: TROKIN, PAUL B.
APPLICANT: TACK, BRIAN
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALITIE OF INVENTION: CATHELICIDINS
TITLE OF INVENTION UNBER: US/10/721,839
CURRENT PILITIG DATE: 2003-11-25
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ORGANISM: Artificial Sequence
FERATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-721-839-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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                                                                                                                                                                  APPLICANT: Tran, Dat Q.

TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
FITLE OF INVENTION: Thereof, and Methods of Use
FILE REFERENCE: 66778-302 (UC5754)
CURRENT APPLICATION NUMBER: US/10/427,715
CURRENT FILING DATE: 2003-04-30
PRIOR PAPLICATION NUMBER: US 60/377,071
PRIOR PAPLICATION NUMBER: US 60/377,071
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: US/10/060,102
PRIOR PILING DATE: 2002-02-22
PRIOR PPLICATION NUMBER: 60/309,368
PRIOR PILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/265,270
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
; CTHER INFORMATION: synthetic construct US-10-427-715-30
                                                                Sequence 30, Application US/10427715
Publication No. US20040014669A1
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tran, Dat Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -10-427-715-30
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LENGTH: 18
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

April 28, 2005, 14:00:51 ; Search time 26 Seconds (without alignments) 66.612 Million cell updates/sec

112 1 GVCRCLCRRGVCRCLCRR 18 US-10-009-317A-33 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		d			SUMMARIES	
Result No.	Score	Query Match	y h Length	DB	ΩI	Description
- H	80	71.4	-	7	C59089	theta defensin-1 -
7	9	53.6	9/ 9		B59089	theta defensin 1b
٣	58	51.8	8 188	~	T15651	hetical pr
4	57		9 164		T24272	
₂	53.5	•	8 419		869207	О
y	52.5	46.	1131		T15617	hypothetical prote
7	52	46.4			T18975	
Φ	51	45.	5 76		A59089	
6	51	45.	5 .85		T48125	hypothetical prote
10	50.5	45.	1 582		B45878	hypothetical prote
11	20		6 131		S50807	probable membrane
12	49.5				E71602	probable integral
13	49	•			JC5042	G protein-coupled
14	48	42.	9 290		G72858	AcOrf-70 protein -
15	48	٠	σ.		B70554	hypothetical prote
16	48		9 1217		EGMSMG	epidermal growth f
17	47.5	٠	4 265		A41116	₽
. 18	47	42.0			S08167	Balbiani ring 3 pr
19	47	42.0			GNNY21	genome polyprotein
20	47	٠	5		T42214	otogelin - mouse
21	٠	41.	5 77		148725	Q300 protein - mou
22	46.5		~		T46871	C-8 sterol isomera
23	ė.		a o		JP0076	nel protein - chic
24	46	41.	1 53		S29214	neurotoxin Tx2 - 8
25	46	41.	1 79		LNPG1	pulmonary surfacta
56	46	41	1 94	•	C37057	fibronectin recept
27	46	41.1	128	•	D72481	hypothetical prote
28	46	41	302	~	A25854	chloramphenicol re
29	46	41	1 321		H90942	probable diogenase

probable dioxygena probable diogenase	cobyric acid synth epidermal growth f	restrictin precure proteinase inhibit	Bowman-Birk protei	proteinase inhibit hypothetical prote	hypothetical prote	probable dioxygena	probable cobQ prot	protein F12K21.20	fibronectin recept	hypothetical prote	hypothetical prote
C64941 D85791	C82426 EGRT	JH0675 S07405	JC2225	TISYC2 T28784	S02186	AE0304	C70940	H86468	B27079	T15840	S26689
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414	41.1	41.1	40	404	40	40	40	40	40	40	39
46 46	4 4 4 6	46 45.5	45.5	45 5.5	45	45	45	45	45	45	44.5
30	35 33	34 35	36	337	39	40	41	42	43	44	45

ALIGNMENTS

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C;Species: Macaca mulatra (rhesus macaque)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: C59089
R;Tang, Y; Q; Yuan, J; Osapay, G; Osapay, K.; Tran, D.; Miller, C.J.; Ouellette, A.J. Science 286, 498-502, 1999
A;Title: A cyclic antimicrobial peptide produced in primate leukocytes by the ligation A;Reference number: A59089; MUID:99453140; PMID:10521339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A. Accession: C59089
A. Status: preliminary
A. Status: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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theta defensin-1 - rhesus macaque
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Matches 12; Conservative
                                                                              N;Alternate names: RTD-
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A)Cromment: For the complete mature sequence, see PIR:C59089.

C;Comment: For the complete mature sequence, see PIR:C59089.

C;Superfamily: mammalian defensin

C;Keywords: antibacterial; antibiotic; antifungal; leukocyte; protein splicing

F;1-20/Domain: signal sequence #status predicted <SIG>

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vascular endothelial growth factor C precursor - human
NyAlternate names: FLT4 ligand DHM
C;Species: Homo sapiens (man)
C;Date: 27-Apr-1996 #sequence revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: 562207; 561795; 571443; 569208; G02659
R;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksela, E,Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksela, A;Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand farence number: 569207
A;Reference number: 569207
A;Reference number: 689207
A;Residues: 1-419 <JOUS
A;Residues: 1-410 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Reidues: 'X', 104-120 cJUU2>
A;Reidues: 'X', 104-120 cJUU2>
A;Reidues: 'X', 104-120 cJUU2>
B:Lee, J'; Gray, A.; Yuan, J'; Luoh, S.M.; Avraham, H.; Wood, W.I.
submitted to the EMBL Data Library, December 1995
A;Description: Vascular endothelial growth factor related protein (VRP): A ligand and A;Reference number: $69208
A;Reference number: $69208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Accession: S61795
A,Status: nucleic acid sequence not shown; not compared with conceptual translation
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F;13-102/Domain: propeptide #status predicted <PRO>
F;103-419/Product: vascular endothelial growth factor C #status experimental <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-419 <LEE>
A;Cross-references: EMBL:U43142; NID:gl150988; PIDN:AAA85214.1; PID:gl150989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL: U58111; NID: 91373426; PIDN: AAB02909.1; PID: 91373427
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein C25F6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15617
R;Benlby, D.
submitted to the EMBL Data Library, October 1995
A;Reference number: Z18377
A;Reference number: Z18377
A;Accession: T15617
A;Accession: T15617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 70-419 < UOU1>
A;Note: this sequence has been revised in reference 569207
A;Accession: 871443
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A;Molecule type: mRNA
A;Residues: 1-419 <MOR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 CRCLCRRGV-----CRCLCR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Morris, J.C.
submitted to the EMBL Data Library, May 1996
A;Reference number: H01557
A;Accession: G02659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Gene: GDB:VEGFC; VRP
A,Cross-references: GDB:3890883; OMIM:601528
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A; Reference number: Z19867
A; Accession: T24272
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residue: preliminary;
A; Rolecule type: DNA
A; Residues: 1-164 < WILD.
A; Cross-references: UNIPROT: Q22048; EMBL: Z66499; PIDN: CAA91301.1; GSPDB: GN00020; CESP: TG
A; Experimental source: clone T01B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, May 1996
A;Description: The sequence of C. elegans cosmid C27A2.
A;Reference number: Z18382
A;Accession: T15651
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-188 <NHA>
A;Cross-references: UNIPROT:Q18238; EMBL:U58760; NID:g1330384; PID:g1330389; PIDN:AAB007
A;Experimental source: strain Bristol N2; clone C27A2
C;Genetics:
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein C27A2.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15651
R;Nhan, M.
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                               F;21-64/Domain: amino-terminal propeptide #status predicted <PRO>F;74-76/Domain: carboxyl-terminal propeptide #status predicted <CTP>
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                                                                                                                            DB 2; Length 76;
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2.9;
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Pred. No. 2.9;
0; Mismatches
                                                                                                                               Score 60; DB 2
Pred. No. 0.81;
1; Mismatches
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Pred. No.
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                                                                                                                            Query Match 53.6%;
Best Local Similarity 83.3%;
Matches 10; Conservative 1
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55.6%;
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Best Local Similarity
Matches 10; Conserv
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A; Introns: 20/3; 90/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: CESP:C27A2.5
A;Map position: 2
A;Introns: 19/3; 91/2
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Best Local
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65 RCICTRGFCRLL 76

Matches

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A;Title: A mouse chromosome 17 gene encodes a testes-specific transcript with unusual p A;Reference number: A45878; MUID:89307395; PMID:2568335 A;Accession: B45878
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A;Accession: S50807
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                              hypothetical protein F16M2.210 - Arabidopsis thaliana (Species: Arabidopsis thaliana (Mouse-ear cress) (C.Species: Arabidopsis thaliana (Mouse-ear cress) (C.Species: O.Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004 (C.SAccession: T48125 (C.SAccession: T48125 (C.SAccession: A.S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, Submitted to the Protein Sequence Database, April 2000 (C.S.; Ascession: T48125 (C.S.; Ascession: T48125 (C.S.; Ascession: T48125 (C.S.; Ascession: Asces
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A;Molecule type: mRNA
A;Residues: 1-582 <88NA
A;Residues: 1-582 <88NA
A;Cross-references: UNIPROT:Q62295; GB:M28821
A;Note: this sequence has been corrected in Immunogenetics 31, 283-284 (1990)
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C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: B45878
R;Sarvetnick, N.; Tsai, J.Y.; Fox, H.; Pilder, S.H.; Silver, L.M.
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NiAlternate names: hypothetical protein HRC131; hypothetical protein J1120
Cispecies: Saccharomyces cerevisiae
Cispecies: Saccharomyces cerevisiae
Cipate: 13-Jan-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
Ciaccession: SS0807; S47126; S5838
F:Vandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.
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44.4%; Pred. No. 9.6;
tive 2; Mismatches
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Matches 9; Conservative
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Best Local Similarity
Matches 12; Conserv
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A; Note: F16M2.210
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A;Accesion: T18975
A;Accesion: T18975
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residuae: 1-152 < WILD-
A;Cross-references: UNIPROT:Q9XVX3; EMBL:Z49886; PIDN:CAA90055.1; GSPDB:GN00020; CESP:CC
A;Experimental source: clone C06A1
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A.Title: A cyclic antimicrobial peptide produced in primate leukocytes by the ligation c A.Reference number: A59089; MuID:99453140; PMID:10521339
A.Accession: A59089
A.Cross-references: UNIPROT:P82270; GB.AF191100; NID:96137227; PIDN:AAF04389.1; PID:9613
C.Comment: For the complete mature sequence, see PIR:C59089
C.Superfamily: mammalian defensin
C.Superfamily: mammalian defensin
C.Superfamily: animbacterial, antibiotic; antifungal; leukocyte; protein splicing
F.1-20/Domain: signal sequence #status predicted <SIGS
F.1-24/Domain: animo-terminal propeptide #status predicted <PRO>
A;Molecule type: DNA
A;Residues: 1-1131 <BEN>
A;Cross-references: EMBL:U39742; NID:g1049455; PID:g1049459; PIDN:AAA80434.1; CESP:C25F6
C;Genetics:
A;Gene: CESP:C25F6.2
A;Gene: CESP:C25F6.2
A;Introns: 105/1; 210/3; 283/3; 316/1; 346/2; 463/3; 566/1; 722/2; 897/1; 991/2; 1032/1;
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; Superfamily: mammalian defensin
; Reywords: antibacterial; antibiotic; antifungal; leukocyte; protein splicing
;1-20/Domain: signal sequence #status predicted <SIG>
;21-64/Domain: amino-terminal propeptide #status predicted <PRO>
;21-64/Domain: amino-terminal propeptide #status predicted <PRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein C06Al.6 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C.Accession: T18975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   theta defensin la precursor - rhesus macaque
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 29-Oct_1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 52; DB 2;
Pred. No. 11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.5%; Score 51; DB 2
66.7%; Pred. No. 8.9;
tive 1; Mismatches
                                                                                                                                                                                                                                                                            46.9%; Score 52.5; Dilarity 47.1%; Pred. No. 33; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, June 1995
A, Reference number: Z19054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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Best Local Similarity
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Best Local Similarity
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Best Local Similarity
Matches 9; Conserv
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A;Map position: 2
A;Introns: 22/3
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C, Genetics:

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Matches

5

us-10-009-317a-33.rpr

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228 QCFCPRQGYKCECICRR 244
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Matches 9; Conservative
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nes 8; Conservative
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A;Molecule type: DNA
A;Residues: 1-290 <AYI
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A;Cross-references: UNIPROT: P47038; EMBL: Z34288; NID: 9498992; PIDN: CAA84058.1; PID: 94990
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994
K;Vandenbol, M:, Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.
submitted to the EMBL Data Library, June 1994
A;Description: Sequence analysis of a 17.1 kb DNA fragment from chromosome X of Sacchard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Accession: JC5042
R,Isoai, A.; Kawahara, H.; Okazaki, Y.; Shizuri, Y.
Gene 175, 95-100, 1996
A;Title: Molecular cloning of a new member of the putative G protein-coupled receptor A;Reference number: JC5042; MUID:97074655; PMID:8917082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ij
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C;Species: Balanus amphitrite (barnacle)
C;Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                           A,Reference number: S56835
A,Accession: S56838
A,Accession: S56838
A,Residues: 1-131 <POH>
A,Residues: 1-131 <POH>
C,Cross-references: EMBL:Z49340; NID:g1008212; PID:g1008214; MIPS:YJL064w
A,Cross-references: SGD:S0003600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 10L
C;Superfamily: Saccharomyces probable membrane protein YJL064w
C;Keywords: transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                A,Accession: S47126
A,Molecule type: DNA
A,Residues: 1-131 «VAW>
A,Cross-references: BL:Z34288; NID:g498992; PID:g499002
R,Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F. submitted to the Protein Sequence Database, September 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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44.6%; Score 50; DB

Best Local Similarity 52.9%; Pred. No. 17;

Matches 9; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GVCRCLCRRGVCRCLCR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 ICTCTC---ICSCLC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Experimental source: clone 3D7 C, Genetics: A, Gene: PFB0950w
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                                                                                                              A; Reference number: S47117
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Best Local Similarity
Matches 7; Conserv
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A;Molecule type: DNA
A;Residues; 1-476 <1SO>
A;Residues; 1-476 <1SO>
A;Cross-references: UNIPROT:Q93126; DDBJ:D78363; NID:g1514430; PIDN:BAA11375.1; PID:g15¹
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane #status predicted <TM1>
F;74-57/Domain: transmembrane #status predicted <TM2>
F;74-57/Domain: transmembrane #status predicted <TM3>
F;16-134/Region: G protein-binding #status predicted <TM3>
F;148-172/Domain: transmembrane #status predicted <TM5>
F;199-222/Domain: transmembrane #status predicted <TM5>
F;197-398/Domain: transmembrane #status predicted <TM6>
F;197-340/Domain: transmembrane #status predicted <TM6>
F;177-398/Domain: transmembrane #status predicted <TM6>
F;217-398/Domain: transmembrane #status predicted <TM6>
F;217-398/Domain: transmembrane #status predicted <TM6>
F;217-398/Domain: transmembrane #status predicted <TM6>
F;230,240,250,260/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status F;230,240,250,260/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acorf-70 protein - Autographa californica nuclear polyhedrosis virus C;Species: Autographa californica nuclear polyhedrosis virus, AcMNPV A;Note: dSDNA virus C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004 C;Accession: G72658 R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D. A;Iriology 202, 586-605, 1994 A;Iriology 202, 586-605, MUD: Autographa californica nuclear polyhedrosis virus A;Reference number: A72850; MUD: 94303173; PMID: 8030224
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C; Species: Mycobacterium tuberculosis
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C; Accession: B70554
R; Davies, R: Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, V.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, V.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, V.; Rutter, S.; Seeger, K.; Whitehead, S.; Barrell, B.G.
A; Atlie: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID:98295987; PMID:9634230
A; Accession: B70554
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-303 <COL>
A; Residues: 1-303 <COL>
A; Residues: 1-303 <COL>
A; Experimental source: strain H37Rv
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C;Genetics:
A;Gene: Rv1145
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0; Gaps Query Match Best Local Similaritý 60.0%; Pred. No. 48; Matches 9; Conservative 0; Mismatches 6; Indels

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Search completed: April 28, 2005, 14:22:38 Job time: 27 secs

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brachydanio caenorhabdi

drosophila

Run on:

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10; Conservative
                                                                                                                                                     PRELIMINARY;
462
152
1526
23015
23015
104
134
2327
2327
2327
628
628
                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
SMART; SM00109;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                            Q6ZMP3;
                                                                                                                                                                                                                                                                                                                                                                                          Kinase
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TD1B_MACMU
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                                                                                                                                       RESULT 1
Q6ZMP3
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homo sapien
anopheles g
caenorhabdi
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homo sapien
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caenorhabdi
caenorhabdi
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caenorhabdi
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                                              April 28, 2005, 13:58:25 ; Search time 114 Seconds (without alignments) 80.855 Million cell updates/sec
                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                               Q6p8t4
Q8ch20
Q8ch20
Q1823k
Q1823k
Q95qy1
Q1764i
Q9566
Q9566
Q6cy99
Q7wv7
Q8ihd6
Q7wv7
Q8ihd6
Q7mv7
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Q9h9u3 |
Q9w0a0
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Q7yuu2
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Q9h654
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Q9d9i2
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                                                                                                                                              1612378
        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                1612378 segs, 512079187 residues
                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                          Q6ZMP3
TD1B_MACMU
Q9D9<u>T</u>2
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Q6FH59
                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                   OM protein - protein search, using sw model
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Q8CH20
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018238
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Q95QY1
Q17641
Q949G1
Q9UI23
Q69566
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Q6ZQS2
Q7PDW6
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Q8IMJ2
Q7SXV0
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Q6R5G9
Q8BPC0
Q9H654
                                                                             US-10-009-317A-33
112
1 GVCRCLCRRGVCRCLCRR 18
                                                                                                                 Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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56.5
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Maximum DB
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Result

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drosophila
anopheles g
mus musculu
                                                                                                              homo sapien
xenopus lae
                                                                                                                                                   macaca mula
arabidopsis
                                                                                                                                                                                        macaca fasc
sinorhizobi
                                                                                                                                                                                                                           mus musculu
burkholderi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB-TONGUE;

TISSUB-TONGUE;

Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F., Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T., Irie R., Oteuki T., Sato H., Wakamateu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Watsuo K., Nishikawa T., Kimura K., Wagateuma M., Murakawa K., Ranehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuhtted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

HSSP: P09215; IBDY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TDIB MACMU STANDARD; PRT; 76 AA.
P8271;
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Theta defensin-1, subunit B precursor (RTD-1b) (Demidefensin 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3,
                   09x7x3 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cascade; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 AA; 27566 MW; 23D41825EB9F782D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Hypothetical protein FLJ16784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.0%; Score 60.5; DB 66.7%; Pred. No. 3.1; iive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0007242; P:intracellular signaling
InterPro; IPR008973; C2 CalB.
InterPro; IPR02219; DAG_PB-bind.
                                                                                                                                                                                                                                                                                                     ALIGNMENTS
06GQP2
Q9XVX3
Q9XVX3
Q8IQ18
Q8IQ18
Q7PG24
Q8PW14
Q8N962
Q91BG7
Q91BG7
Q91BG7
Q9MVJ6
Q8MKJ2
Q8MKJ2
Q8COH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE, PS50081; DAG_PE_BIND_DOM_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00130; C1 1; 1. PRINTS; PR00008; DAGPEDOMAIN.
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SEQUENCE FROM N.A.

RC Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

RA Adachi J., Aizawa K., Akahira S., Fukunishi Y., Furuno M.,

A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

RA Arakawa T., Kojima Y., Kono M., Hiramoto K., Hiraoka T., Kato H.,

RA Mat J., Kojima Y., Kono H., Koda M., Koya S., Kurihara C.,

RA Adai J., Kojima Y., Kono H., Koda M., Koya S., Kurihara C.,

RA Adai J., Kojima Y., Kohino H., Koda M., Koya S., Kurihara C.,

RA Asaaki Y., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

Rano H., Sasaki D., Shibata K., Shibata Y., Shinaqawa A., Takahashi T.,

Rogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

Rogabe Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

Muramatsu M., Hayashizaki Y.;

Rubmitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

RGD, MGI:1913992; 4931420D14Rik.

W Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A.
SETRAM=CS7BL/G07 TISSUE=Testis;
MEDLINE=CS7BL/G17 TISSUE=Testis;
MEDLINE=20499374; PubMedl1042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Monno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Monno H., Okazaki Contraction of cap-trapper-selected cDNAs to
prepare full-length cDNA lbraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                              STRAIN=CS7BL/64; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/64; TISSUE=Testis;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Matsunai T., Tashiro H., Itoh M., Sumi N., Ishira Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunai S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsuninoto H., Sakaguchi S., Ikegami T., Kashiiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watsuhiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rike integrated sequence and Y. Kira A., Hayashizaki Y.; Rike integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:1700055105 product:hypothetical Cysteine-rich region
Containing protein, full insert sequence.
Name-4931420D14Rik;
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J, TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The FANTOM Consortium,
                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                SEQUENCE FROM N.A., SEQUENCE OF 65-73, TISSUE SPECIFICITY,
DEVELOPMENTAL STAGE, AND DISULFIDE BONDS.
TISSUE=Bone marrow, and Leukocyte;
MEDLINE=99453140; PubMed=1051339; DOI=10.1126/science.286.5439.498;
Tang Y.-Q., Yuan J., Osapay G., Osapay K., Tran D., Miller C.J.,
Ouellette A.J., Selsted M.E.;
"A cyclic antimicrobial peptide produced in primate leukocytes by the
ligation of two truncated alpha-defensins.";
Science 286:498-502(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

TISSUE-Bone marrow;
Zhao C., Nguyen T., Lehrer R.I.;
Zhao C., Nguyen T., Lehrer alpha-defensins and three demidefensins from "cDNA cloning of three alpha-defensins and three monkey bone marrow.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Active against Gram-positive bacteria S.aureus and L.monocytogenes, Gram-negative bacteria S.typhimurium and B.coli ML3S and fungi C.albicans and C.neoformans in vitro.
-!- SUBUNIT: Forms a cyclic heterodimer composed of subunits A and B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disulfide-linked.
--- TISSUE SPECIFICITY: Expressed in bone marrow. Detected in promyelocytes, myelocytes and mature neutrophils and monocytes.
---- DEVELOPMENTAL STAGE: Expression begins early during granulocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPRU02200, Thropep; 1.
PROSTE; PS00269; DEFENSIN; FALSE NEG.
PROSITE; PS00269; DEFENSIN; FALSE NEG.
Antibiotic; Defensin; Direct protein sequencing; Fungicide; Signal.
22 Potential.
                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               À
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       With this is a cyclic peptide.
SIMILARITY: Belongs to the corticostatin/defensin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Theta defensin-1, subunit B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F0B754466156071E CRC64;
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Pred. No. 1.3;
1; Mismatches
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Q9D912 PRELIMINARY; PRT;
AC Q9D912; TrEMBLrel 17, Created)
DT 01-JUN-2001 (TrEMBLrel 17, Created)
                                 Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF191101; AAF04390.1; -.
EMBL; AF191103; AAF04392.1; -.
EMBL; AF184156; AAF07923.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                           Cercopithecinae; Macaca.
NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; B59089; B59089
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65
74
66
68
76 AA;
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SEQUENCE Query Match

Best Loca Matches

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DISULFID PEPTIDE PROPEP

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Gaps

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us-10-009-317a-33.rup

g

RESULT 4

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STRAIN=C57BL/6J; TISSUE=Testis; MEDLINE=20499374; Pubmed=11042159; DOI=10.1101/gr.145100; MEDLINE=20499374; Pubmed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(200).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninol P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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01-002-2002 (TrEMBLrel. 22, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
11brary, clone:4931420014 product:hypothetical Cysteine-rich region
Name=4931420014Rik;
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STRAIN=C57BL/6J; TISSUE=Testis;
The FANTOW COnsortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation
                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                             STRAIN=CD-1; TISSUE=Testis; Xu X., Bai X., Silvius D., Escalier D., McFarland L., Xu P.-X.; Submitted (DEC-2201) to the EMBL/GenBank/DDBJ databases. EMBL; AF465502; AAO15675.1; MGD; MGD; MGI:1913992; 4931420D14Rik. SEQUENCE 168 AA; 18957 MW; 8F30D3D27B9BF595 CRC64;
                                                                                                                                                                                                                                                                                                                                                                  51.8%; Score 58; DB 2; Length 168; 56.2%; Pred. No. 4.6; 7; Indels tive 0; Mismatches 7; Indels
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STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 AA.
       Name=4931420D14Rik; Synonyms=Cktlr3;
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                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                             NCBI_TaxID=10090;
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Q9D4K2;
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Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                     Length 168;
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Director MGC Project;
Director MGC Project;
Director MGC Project;
EMBL/GenBank/DDBJ databases.
EMBL; BC061079; AA461079.1;
SROUENCE 168 AA; 18947 MW; BO0FD3D27B9BF768 CRC64;
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18931 MW; 7A2BD279612A5E94 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last sequence update)
Last annotation update)
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                                                     DB 2;
                                                  53.6%; Score 60; DB 2 '56.2%; Pred. No. 2.6; ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                          168 AA.
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               4931420D14Rik protein.
                     Query Match
Best Local Similarity '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
168 AA;
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Matches 9; Conserv
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SEQUENCE
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Q8CH20;
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Local Similarity 55.6
hes 10; Conservative
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                  Wilson R.;
Submitted (JUN-2004)
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   STRAIN-Bristol N2;
                                                                  SEQUENCE FROM N.A. STRAIN=Bristol N2;
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01-NOV-1996
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C STRAIN=C57ENL/64); TISSUE=Testis;
A Arakawa T., Akahira S., Akimura T., Arai A., Aono H.,
A Arakawa T., Bono H., Carninci P., Fukuda S., Pukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiramcto K., Hiraoka T., Hori F.,
A Managaki T., Hara A., Hayatsu N., Hiramcto K., Hiraoka T., Hori F.,
A Managaki T., Kano H., Konda M., Koya S., Kurihara C.,
A Kawai J., Kojima Y., Konno H., Koya M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
A Sano H., Sasaki D., Shibata Y., Shibata Y., Shinagawa A., Shizaki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yoneda X., Inoue K., Togawa Y., Izawa M., Ohara E., Warahiki M., Yoneda X., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEW integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mornhase Consortium, Wormhase Consortium, "Genome sequence of the nematode C. elegans: a platform for "merinating biology. The C. elegans Sequencing Consortium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.8%; Score 58; DB 2; Length 173; 56.2%; Pred. No. 4.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The sequence of C. elegans cosmid C27A2."; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AKO16467; BAB30253.1;

MGD; MGT:1913992; 4931420D14Rik.

Hypothetical protein.

SEQUENCE 173 AA; 19581 MW; 14786F155AC29FDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein C27A2.5.
Name-C27A2.5; ORFNames=C27A2.5;
Caenorhabditis elegans.
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MEDLINE=99069613; PubMed=9851916;
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Science 282:2012-2018(1998).
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Best Local Similarity 56.2?
Matches 9; Conservative
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SEQUENCE FROM N.A.
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Rhabditidae; Peloderinae; Caenorhabditis.
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GO; GO: 0005576; C: extracellular; IEA.
GO; GO: 0005576; C: extracellular; IEA.
GO; GO: 0005613; P: defense response; IEA.
InterPro; IPR001450; 4Fe4S ferredoxin.
InterPro; IPR001007; WWP C.
PROSITE; PS00198; 4Fe4S FERREDOXIN; UNKNOWN 1.
PROSITE; PS00269; DEFENSIN; 1.
PROSITE; PS01269; WWP C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.8%; Score 58; DB 2; Length 188; 55.6%; Pred. No. 5.1;
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Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; Z66499; CAA91301.1; -.
PIR; T24272; T24272.
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to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                  WormBase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; US9760; AAK31463.1; -.
PIR; T15651; T15651.
HSSP; P10968; 2CWG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein. TSEQUENCE 188 AA; 18878 MW; 0C5D0DC5CA8E0C4B CRC64;
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Wormbep; T01B7.8; CB03592.
InterPro; IPR0061450; 4Fe45_ferredoxin.
InterPro; IPR006081; Defensin_alpha.
InterPro; IPR006209; EGF_like.
InterPro; IPR001007; WWF_C.
INCOSTIE; PS00108; 4FE45_FERREDOXIN; UNKNOWN_1.
PROSTIE; PS00269; DEFENSIN; UNKNOWN_1.
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STRAIN-Bristol N2;
MEDLINE-99069613; Pubmed-9851916;
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ORFNames=T01B7.8;
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2004 (TrEMBLrel. 26,
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                      Length 164;
                                                                           8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Bristol N2;
Anderson K., Chissoe S.;
"The sequence of C. elegans cosmid C04G6.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
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                     Hypothetical protein. --
SEQUENCE 164 AA; 16499 MW; C002D48D36C9FCED CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mypothetical protein C04G6.10.
Name=C04G6.10; ORFNames=C04G6.10;
Caenorhabditis elegans.
                                                    Query Match 50.9%; Score 57; DB 2; Best Local Similarity 55.6%; Pred. No. 6; Matches 10; Conservative 0; Mismatches
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PROSITE; PS00269; DEFENSIN; UNKNOWN 1.
PROSITE; PS00022; EGF 1; UNKNOWN 1.
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WormPep; C04G6.10; CE27649.
InterPro; IPR001450; 4Fe48 ferredoxin.
InterPro; IPR006081; Defensin_alpha.
InterPro; IPR006209; EGF like.
InterPro; IPR001007; VWF_C.
PROSITE, PS00022; EGF 1; UNKNOWN 1.
PROSITE, PS01208; VWFC 1; UNKNOWN 1.
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PROSITE; PS01208; VWFC 1; UNKNOWN Hypothetical protein. SEQUENCE 166 AA; 16971 MW; 9D9
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MEDLINE=99069613; PubMed=9851916;
                                                                                               1 GVCRCLCRRGVCRCLCRR 18
                                                                                                                   GGCGCCCRPRCCCCRR 97
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Best Local Similarity
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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  Indels
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Anderson K., Chissoe S.;
"The sequence of C. elegans cosmid C04G6.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; U55854; AAK68161.1; -.
HSRP; P10969; 1WGT.
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
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Mismatches
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InterPro; IPR006081; Defensin_alpha.
InterPro; IPR006209; EGF like.
InterPro; IPR001007; WWF_l.
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MEDLINE=99069613; PubMed=9851916;
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Name=C04G6.7; ORFNames=C04G6.7;
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                                          1 GVCRCLCRRGVCRCLCRR 18
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Matches 10; Conservative
10; Conservative
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SEQUENCE 197 AA; 2
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01-OCT-2001
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Q17641
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Length 166;

DB 2;

0949G1

RESULT 11 Q949G1

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MEDLINE=9133007; PubMed=1651403;
Teo 1.A., Griffin B.E., Jones M.D.; "Characterization of the DNA polymerase gene of human herpesvirus 6.";
J. Virol. 65:4670-4680(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Martin M.E.D., Nicholas J., Thomson B.J., Newman C., Honess R.W.; "Identification of a transactivating function mapping to the putative immediate-early locus of human herpesvirus 6.";
                                                                                                                                                                                                                                Littler B., Lawrence G., Liu M.Y., Barrell B.G., Arrand J.R., ardentification, cloning, and expression of the major capsid protein gene of human herpesvirus 6.";
                                                                                                                                                                                                                                                                                                                                                                                                                       "Human herpesvirus 6 is closely related to human cytomegalovirus.";
J. Virol. 64:287-299(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chang C.K., Balachandran N.; "Identification, characterization, and sequence analysis of a cDNA encoding a phosphoprotein of human herpesvirus 6."; J. Virol. 65:2884-2894(1991).
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MEDLINE=22260671; PubMed=1374813;
Neipel F., Ellinger K., Fleckenstein B.;
"Gene for the major antigenic structural protein (p100) of human
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-90080132; PubMed-2152817;
Lawrence G.L., Chee M., Craxton M.A., Gompels U.A., Honess R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91226542; PubMed=1851252; DOI=10.1038/351078a0;
                                                                                                         RNA stage; Herpesviridae;
               Last sequence update)
Last annotation update)
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MEDLINE=91374590; PubMed=1654446;
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                                                                                      Human herpesvirus 6.
Viruses; dsDNA viruses, no RNA s!
Betaherpesvirinae; Roseolovirus.
NCBI_TaxID=10368;
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J. Virol. 66:3918-3924(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human herpesvirus type-6.";
Nature 351:78-80(1991).
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                   (TrEMBLrel. (TrEMBLrel.
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01-OCT-2002
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 01-NOV-1996
                                                                        Name=U88;
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                                                                                                                                                                                                                                                                       MEDLINE=21329048; PubMed=11435398; DOI=10.1101/gr.GR-1617R; Mayer K., Murphy G., Tarchini R., Wambutt R., Volckaert G., Pohl T. Duesterhoeft A., Stiekema W., Entian K.D., Terryn N., Lemcke K., Haase D., Hall C.R., van Dodeweerd A.M., Tingey S.V., Mewes H.W., evan M., Bancroft I.; Comparation of microstructure bewtween a sequenced region of the genome of rice and multiple segments of the genome of Arabidopsis thaliana.";
                                                                                                                                                                     Oryza sativa (Rice).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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55.6%; Pred. No. 7.8;
:ive 2; Mismatches 3; Indels 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.9%; Score 57; DB 2; Length 274; 60.0%; Pred. No. 9.3;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Gramene; Q949G1; -.
Hypothetical protein.
SEQUENCE 274 AA; 28657 MW; ABS47D9BDS470AE1 CRC64;
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Last sequence update)
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                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein C15ERIPDM.
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Query Match

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Jones M., Teo I.; "Identification and analysis of the transport/capsid assembly protein (tp/cap) gene of human herpesvirus-6 (HHV-6)."; virology 197:449-454(1993).
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A strongly immunoreactive virion protein of human herpesvirus 6 variant B strain 229: identification and characterization of the ge and mapping of a variant-specific monoclonal antibody reactive
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Thompson J., Choudhury S., Kashanchi F., Doniger J., Berneman Z., Frenkel N., Rosenthal L.J.;
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"The right end of the unique region of the genome of human herp, 6 Ullo2 contains a candidate immediate early gene enhancer and homologue of the human cycomegalovirus US22 gene family.";
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Fleckenstein B.;
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MEDLINE=93187613; PubMed=8383182;
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Virology 195:521-531(1993)
[17]
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(1] — SEQUENCE FROM N.A.

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(2) Fanebori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S., Kanehori K., Ishibashi T., Chiba S., Ono Y., Hotuta T., Watanabe M., Sugiyama T., Irle R., Otsuki T., Sato H., Wakamatsu A., Ishi S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., A Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Nagateuma M., Takhashi-Fujii A., Soshina A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahuki K., Magai K., Isogai T.; Submitted (UUL-2003) to the EMBL/GenBank/DDBJ databases.

REBL: AK128797; BAC87611; --

REBL: AK128797; BAC87611; --

REPRO: PRO06209; EGF 1ike.

REPRO: PRO06209; EGF 2; UNKNOWN 1.

REPRO: PROSITE; PSO1186; EGF 2; UNKNOWN 1.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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49.6%; Score 55.5; DB 2; Length 512;
Best Local Similarity 64.7%; Pred. No. 25;
Matches 11; Conservative 1; Mismatches 4; Indels
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49.1%; Score 55; DB 2; Length 201;
Best Local Similarity 53.3%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 5; Indels
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                                                                                                                                                                                                                                                             endogenous neuromodulator gamma-hydroxybutyrate.";

FASEB J. 0.0-0(2004).

EMBL; AY48533; AAR24072.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:00164872; F:receptor activity; IEA.

InterPro; IPR001209; Ribosomal S14.

InterPro; IPR001031; Transmem_4.

PRINTS; PR00259; TWFOUR.

PROSITE; PS00527; RIBOSOMAL_S14; UNKNOWN_1.
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                                                                                                                  STRAIN-Wistar; TISSUE-Hippocampus;
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NCBI_TaxID=10116;
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SEQUENCE
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